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OM protein - protein search, using sw model

Run on: February 24, 2005, 07:21:27 ; Search time 70 Seconds
(without alignments)
215.481 Million cell updates/sec

Title: US-10-009-473-2
Sequence: 1 KQIIMMGEVGMAYATRPNNYKRIHIGPGRFYTTK 39

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues
Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: A_Geneseq_16Dec04:*
2: geneseqp1980s:*
3: geneseqp1990s:*
4: geneseqp2000s:*
5: geneseqp2001s:*
6: geneseqp2002s:*
7: geneseqp2003s:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	213	100.0	39	AAW32957	C3-V3 MN
2	213	100.0	39	AAW32957	C3-V3 MN
3	213	100.0	39	AAW32957	C3-V3 MN
4	213	100.0	39	AAW32957	C3-V3 MN
5	213	100.0	39	AAW32957	C3-V3 MN
6	202.5	95.1	40	AAW32957	C3-V3 MN
7	202.5	95.1	40	AAW32957	C3-V3 MN
8	202.5	95.1	40	AAW32957	C3-V3 MN
9	202.5	95.1	40	AAW32957	C3-V3 MN
10	202.5	95.1	40	AAW32957	C3-V3 MN
11	202.5	95.1	40	AAW32957	C3-V3 MN
12	202.5	95.1	40	AAW32957	C3-V3 MN
13	202.5	95.1	40	AAW32957	C3-V3 MN
14	202.5	95.1	40	AAW32957	C3-V3 MN
15	202.5	95.1	40	AAW32957	C3-V3 MN
16	202.5	95.1	40	AAW32957	C3-V3 MN
17	202.5	95.1	40	AAW32957	C3-V3 MN
18	202.5	95.1	40	AAW32957	C3-V3 MN
19	202.5	95.1	40	AAW32957	C3-V3 MN
20	194.5	91.3	40	AAW32957	C3-V3 MN
21	194.5	91.3	40	AAW32957	C3-V3 MN
22	194.5	91.3	40	AAW32957	C3-V3 MN
23	194.5	91.3	40	AAW32957	C3-V3 MN
24	194.5	91.3	40	AAW32957	C3-V3 MN
25	194.5	91.3	40	AAW32957	C3-V3 MN

26	187	87.8	39	AAW32964	C3-V3 JRF
27	184	86.4	39	AAW32960	C3-V3 JRF
28	184	86.4	39	AAW32962	C3-V3 BAL
29	182	85.4	39	AAW32963	C3-V3 JRC
30	180	84.5	39	AAW32973	C3-V3 ADA
31	179	84.0	39	AAW32972	C3-V3 HAN
32	178	83.6	39	AAW32965	C3-V3 OYI
33	176	82.6	39	AAW32966	C3-V3 SF2
34	176	82.6	39	AAW32967	C3-V3 SF2
35	176	82.6	39	AAW32968	C3-V3 SF2
36	175	82.2	39	AAW32961	C3-V3 ALA
37	174.5	81.9	35	AAW16527	Peptide (
38	174.5	81.9	35	ABO01835	HIV MN en
39	174.5	81.9	47	AAW40202	Sequence
40	174.5	81.9	47	AAW16529	Peptide (
41	174.5	81.9	47	ABO01837	HIV MN en
42	173	81.2	39	AAW32958	C3-V3 BRV
43	170	79.8	39	AAW32959	C3-V3 SC
44	170	79.8	39	ABP59725	HIV immun
45	170	79.8	39	ABP59725	HIV immun

ALIGNMENTS

RESULT 1
ID AAW32957 standard; peptide; 39 AA.
AC AAW32957;
DT 23-JAN-1998 (first entry)
DE C3-V3 MN immunogen construct.
XX
XX Immunogen; antigenic determinant; HIV; envelope; glycoprotein; env; gp;
XX recognition; B lymphocyte; type specific; antibody; vaccine; protection;
XX immune response; infection; neutralisation.
XX
XX Human immunodeficiency virus;
XX Synthetic.
XX W05714436-A1. = U.S. Patent No. 5,993,819.
XX 24-APR-1997.
XX
XX 18-OCT-1996; 96WO-US016911.
XX
XX 20-OCT-1995; 95US-00546515.
XX 09-FEB-1996; 96US-00599266.
XX
XX (UYDU-) UNIV DUKE.
XX
XX Haynes BF, Palker TU;
XX WPI; 1997-244662/22.
XX
XX Synthetic human immunodeficiency virus vaccine - comprising hydrophilic
XX peptide corresponding to at least 1 antigenic determinant of envelope
XX glyco:protein recognised by B lymphocytes.
XX
XX Example 11; Page 60j; 104pp; English.
XX
XX The present sequence, which comprises at least 1 antigenic determinant of
XX human immunodeficiency virus (HIV) envelope (env) glycoprotein (gp)
XX recognised by B lymphocytes, when covalently linked to a carrier
XX molecule, induces the production of high titres of protective, type
XX specific anti-HIV antibodies (Ab) in a mammal. The peptide can be used in
XX vaccines for producing a protective immune response to HIV infection,
XX while a HIV neutralising Ab can be induced in a primate by administering
XX a composition comprising HIV env peptides that disrupt gp120/gp41
XX interactions

SQ Sequence 39 AA;

Query Match 100.0%; Score 213; DB 2; Length 39;
 Best Local Similarity 100.0%; Pred. No. 4.2e-19;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Dy 1 KOIINMGEVGMKATRPNNKRRKRIHIGRAFYTTK 39
 Db 1 KOIINMGEVGMKATRPNNKRRKRIHIGRAFYTTK 39

RESULT 2

ID AAB49387 standard; peptide; 39 AA.

AC AAB49387;

DT 06-MAR-2001 (first entry)

DE HIV peptide SEQ ID NO: 2.

KW HIV, immunogenic peptide; immune response; monophosphoryl lipid A;
 KW antigen; infection; cancer; amyloid deposition.
 OS Human immunodeficiency virus.

FN WO200069456-A2.

PD 23-NOV-2000.

PF 12-MAY-2000; 2000WO-US013156.

PR 13-MAY-1999; 99US-0133963P.

PA (AMCY) AMERICAN CYANAMID CO.

PI Hagen M;

DR WPI; 2001-024946/03.

PT Antigenic composition having an antigen (e.g. viral protein) and an
 PT adjuvant, useful for enhancing humoral and cellular immune response in a
 PT host or as a prophylaxis against virus, bacterium, parasite, cancer cell
 or allergen.

PS Claim 20; Page 109; 129pp; English.
 CC The present invention provides an antigenic composition comprising an
 CC antigen with a 3-O-deacetylated monophosphoryl lipid A or monophosphoryl
 CC lipid A adjuvant. The presence of the adjuvant causes an increased immune
 CC response. The antigen may be from a pathogenic bacterium, fungus, virus
 CC or parasite, a cancer cell, an allergen or from amyloid peptide protein.
 CC The composition can be used in the prevention and treatment of infection,
 CC cancer and diseases caused by amyloid deposition. It is particularly
 CC useful against HIV, Neisseria gonorrhoeae and respiratory syncytial virus

SQ Sequence 39 AA;
 Query Match 100.0%; Score 213; DB 4; Length 39;
 Best Local Similarity 100.0%; Pred. No. 4.2e-19;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Dy 1 KOIINMGEVGMKATRPNNKRRKRIHIGRAFYTTK 39
 Db 1 KOIINMGEVGMKATRPNNKRRKRIHIGRAFYTTK 39

RESULT 3

ID AAB12546

AAU12546 standard; peptide; 39 AA.

AC

XX

XX

DT 11-SEP-2003 (revised)
 DT 27-SEP-2001 (first entry)
 XX
 XX

DE HIV polyvalent C4-V3 peptide C4-V3MN.

KW Human immunodeficiency virus; HIV; immunogen; vaccine; anti-HIV;
 KW human leukocyte antigen; HLA; T-helper epitope; CTL; Th; epitope;
 KW major histocompatibility complex; MHC; cytotoxic T-lymphocyte;
 KW Vaccinia ankara.

OS Human immunodeficiency virus 1.
 FN WO200156355-A2.

PD 09-AUG-2001.

PF 05-FEB-2001; 2001WO-US003540.

PR 04-FEB-2000; 2000US-00497497.

PA (UYDU-) UNIV DUKE.

PI Haynes BF, Liao H;

DR WPI; 2001-488827/53.

PT Vaccine for immunizing against human immunodeficiency virus has mixture
 PT or linear array of peptides comprising immunodominant T-helper epitopes
 PT and major histocompatibility complex cytotoxic T-lymphocyte epitopes.
 PS Disclosure; Page 28; 33pp; English.

CC The present invention relates to human immunodeficiency virus (HIV) and
 CC in particular to a human leukocyte antigen (HLA)-based HIV vaccine. The
 CC vaccine comprises a mixture or linear array of peptides, or its variants,
 CC where the peptides contain immunodominant T-helper (Th) epitopes and
 CC major histocompatibility complex (MHC) cytotoxic T-lymphocyte (CTL)
 CC epitopes and the linear array of peptides are preferably expressed in
 CC modified Vaccinia ankara. The vaccine is useful for immunizing a patient
 CC against HIV and focuses immune response on many dominant and subdominant
 CC CTL epitopes of HIV. DNA or live vectors with linear arrays of CTL
 CC epitopes can be used as either primes or boosts of peptides or of each
 CC other to optimally give CTL anti-HIV responses. The vaccine induces
 CC salutory anti-HIV immune responses. AAU12447-AAU1258 represent the amino
 CC acid sequences of the Th-CTL epitopes and HIV immunogenic peptides used
 CC in the invention. (Updated on 11-SEP-2003 to standardise OS field)

SQ Sequence 39 AA;

Query Match 100.0%; Score 213; DB 4; Length 39;
 Best Local Similarity 100.0%; Pred. No. 4.2e-19;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Dy 1 KOIINMGEVGMKATRPNNKRRKRIHIGRAFYTTK 39
 Db 1 KOIINMGEVGMKATRPNNKRRKRIHIGRAFYTTK 39

RESULT 4

ID AAE26076

AAE26076 standard; peptide; 39 AA.

AC AAE26076;

XX

XX

XX

XX

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XX

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XX

XX

XX

XX

XX

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XX OS Human immunodeficiency virus 1.
XX PN MO200238177-A2.
XX PD 16-MAY-2002.
XX PF 08-NOV-2001; 2001MO-US046943.
XX PR 10-NOV-2000; 2000US-0247100P.
XX PR 18-OCT-2001; 2001US-0330345P.
XX PA (AMCY ) AMERICAN CYANAMID CO.
XX PI Hagen M;
XX DR WPI; 2002-636409/68.
XX PT Antigenic composition for use in enhancing immune response of antigen,
XX PT has selected antigen, and combination of adjuvant comprising an
XX PT aminoalkyl glucosamine phosphate compound, and cytokine or lymphokine.
XX PS Claim 14; Page 71; 94pp; English.
XX CC The invention relates to an antigenic composition comprising a selected
XX CC antigen from a pathogenic virus, bacterium, fungus or parasite, or from a
XX CC cancer or tumour cell, or from an allergen, or from a self molecule; and
XX CC an combination of adjuvant comprising an aminoalkyl glucosamine phosphate
XX CC compound (AGP), or its derivative or analogue, and a cytokine or
XX CC lymphokine, or an agonist to it. The invention is useful for increasing
XX CC the ability of an antigenic composition (enhancing immune response)
XX CC containing a selected antigen from a pathogenic virus, bacterium, fungus
XX CC or parasite to elicit an immune response especially cytotoxic T
XX CC lymphocytes; a selected antigen a cancer or tumour cell to elicit
XX CC therapeutic or prophylactic anti-cancer effect; a selected allergen to
XX CC moderate an allergic response; or a selected antigen from a molecule or
XX CC its portion representing those produced by a host in an undesired manner,
XX CC amount or location so as to reduce an undesired effect, in a vertebrate
XX CC host. The invention is useful for increasing the ability of an antigenic
XX CC composition to prevent or treat disease characterized by amyloid
XX CC deposition in a vertebrate host. The invention is useful as a vaccine.
XX CC The present sequence is HIV-1 peptide, T1SP10MN (A) (-Cys). (Updated on
XX CC 29-AUG-2003 to standardise OS field)
XX SQ Sequence 39 AA:
XX
XX Query Match 100.0%; Score 213; DB 5; Length 39;
XX Best Local Similarity 100.0%; Pred. No. 4, 2e-19;
XX Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 KOIINMDEVGKAMYATRPNNYKRIHIGPGRAFYTTK 39
DB 1 KOIINMDEVGKAMYATRPNNYKRIHIGPGRAFYTTK 39
XX
XX RESULT 5
XX AAU70257
XX ID AAU70257 standard; peptide; 39 AA.
XX AC AAU70257;
XX DT 14-FEB-2002 (first entry)
XX DE HIV polyvalent C4-V3 peptides prototype vaccine C4-V3MN.
XX XX HIV, human immunodeficiency virus; AIDS; SIV; anti-HIV; virucide;
XX KW acquired immunodeficiency syndrome; simian immunodeficiency virus;
XX KW vaccine; cytotoxic T cell response inducer; Th; human leucocyte antigen;
XX KW immunodominant T-helper epitope; cytotoxic T lymphocyte; CTL; HLA.
XX OS Human immunodeficiency virus 1.
XX OS Synthetic.
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PN US2001036461-A1.
XX PD 01-NOV-2001.
XX PF 05-FEB-2001; 2001US-00775805.
XX PR 04-FEB-2000; 2000US-00497497.
XX PA (HAYN/) HAYNES B F.
XX PA (LIAO/) LIAO H.
XX PI Haynes BF, Liao H;
XX DR WPI; 2002-010132/01.
XX PT Vaccine containing overlapping Th-cytotoxic T lymphocyte epitopes, useful
XX PT for protecting against human immune deficiency virus.
XX PS Example 1; Page 8; 11pp; English.
XX CC The invention relates to a vaccine comprising a mixture, or linear array,
XX CC of specific peptides that are human immunodeficiency virus (HIV-1) Th
XX CC (immunodominant T-helper epitope)-cytotoxic T lymphocyte (CTL), or their
XX CC variants. Peptides are also described which contain SIV (simian
XX CC immunodeficiency virus) derived epitopes. The vaccine is used to protect
XX CC against infection by HIV. The vaccines are based on an analysis of HLA
XX CC (human leucocyte antigen) alleles present in subject populations targeted
XX CC for vaccination and the commonest variants of HIV in the locality. They
XX CC contain sufficient immunogenic epitopes to ensure effective presentation
XX CC by almost all members of the target population. The present sequence is
XX CC an HIV-1 epitope based prototype vaccine of the invention
XX SQ Sequence 39 AA:
XX
XX Query Match 100.0%; Score 213; DB 5; Length 39;
XX Best Local Similarity 100.0%; Pred. No. 4, 2e-19;
XX Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 KOIINMDEVGKAMYATRPNNYKRIHIGPGRAFYTTK 39
DB 1 KOIINMDEVGKAMYATRPNNYKRIHIGPGRAFYTTK 39
XX
XX RESULT 6
XX AAR40201
XX ID AAR40201 standard; peptide; 40 AA.
XX AC AAR40201;
XX DT 25-MAR-2003 (revised)
XX DT 05-FEB-1994 (first entry)
XX DE Sequence of peptide construct T1-SP10MN (A) .
XX XX Hybrid protein; synthetic protein; immunogenic peptide; tolerance;
XX KW synthetic toleragen.
XX OS Synthetic.
XX PN WO9315750-A1.
XX PD 19-AUG-1993.
XX PF 10-FEB-1993; 93WO-US001207.
XX PR 10-FEB-1992; 92US-00833429.
XX PA (HAYN/) HAYNES B F.
XX PI Haynes BF;
XX DR WPI; 1993-272554/34.
```

PT Inducing immune tolerance to immunogenic peptide(s) or proteins - by
 PT administering the peptide(s) or proteins coupled to a 2-20 aminoacid
 XX hydrophobic peptide.
 PS Example; Fig 10; 65pp; English.
 CC The peptide is a variant of T1-SP10 peptide derived from HIVMN envelope
 CC sequences. It comprises the following regions from the envelope
 CC sequences: T1, SP10 and A. T1 sequence is AAs 428-443 from HIVMN
 CC SP10MN(A) sequence is AAs 301-319 from HIVMN. (A) sequence is AAs 32-324
 CC from HIVMN and AAs 322-327 from HIVMN. A = additional HIV gp120 V3 loop
 CC an additional neutralising and CTL region to the HIV B cell determinant
 CC of the hybrid peptide. (Updated on 25-MAR-2003 to correct PN field.)
 SQ Sequence 40 AA;

Query Match 95.1%; Score 202.5; DB 2; Length 40;
 Best Local Similarity 97.5%; Pred. No. 8.6e-18;
 Matches 39; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 KOIIMMOEVGKAMVA-TRPNYNNKRRRIHIGPRAFYTTK 39
 1 KOIIMMOEVGKAMVACTRPNNYNNKRRRIHIGPRAFYTTK 40

Db 1 KOIIMMOEVGKAMVACTRPNNYNNKRRRIHIGPRAFYTTK 40

RESULT 7
 AAR40196
 ID AAR40196 standard; peptide; 40 AA.
 AC AAR40196;
 XX
 DT 25-MAR-2003 (revised)
 DT 05-FEB-1994 (first entry)
 XX
 DE Sequence of peptide construct T1-SP10MN(A), type Th-B, derived from HIV
 DE MN and HIVIIIB Env gp120.
 XX
 KW Hybrid protein; synthetic protein; immunogenic peptide; tolerance;
 KW synthetic collagen.
 OS Synthetic.
 XX
 PN MO9315750-A1.
 XX
 PD 19-AUG-1993.
 XX
 PF 10-FEB-1993; 93MO-US001207.
 XX
 PR 10-FEB-1992; 92US-00833429.
 XX
 PA (HAYN/) HAYNES B F.
 XX
 PI Haynes BF;
 XX
 DR WPI; 1993-272554/34.
 XX
 PT Inducing immune tolerance to immunogenic peptide(s) or proteins - by
 PT administering the peptide(s) or proteins coupled to a 2-20 aminoacid
 XX hydrophobic peptide.
 PS Example; Table 8, page 42; 65pp; English.
 CC The peptide composition and sequence (Bp10pe type) of the synthetic
 CC peptide construct is T1(Th) SP10(B cell) and A (B cell). T1 sequence
 CC AAs 428-443 from HIVIIIB. SP10MN(A) sequence is AAs 301-319 from HIVMN.
 CC T helper cell determinant. B cell = B cell neutralising antibody
 CC determinant. A = additional HIV gp120 V3 loop sequences added to the
 CC original synthetic peptide (SP10) sequence to add an additional
 CC neutralising and CTL region to the HIV B cell determinant of the hybrid
 CC peptide. (Updated on 25-MAR-2003 to correct PN field.)

SQ Sequence 40 AA;

Query Match 95.1%; Score 202.5; DB 2; Length 40;
 Best Local Similarity 97.5%; Pred. No. 8.6e-18;
 Matches 39; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 KOIIMMOEVGKAMVA-TRPNYNNKRRRIHIGPRAFYTTK 39
 1 KOIIMMOEVGKAMVACTRPNNYNNKRRRIHIGPRAFYTTK 40

Db 1 KOIIMMOEVGKAMVACTRPNNYNNKRRRIHIGPRAFYTTK 40

RESULT 8
 AAR56981
 ID AAR56981 standard; peptide; 40 AA.
 AC AAR56981;
 XX
 DT 25-MAR-2003 (revised)
 DT 05-MAR-1995 (first entry)
 XX
 DE Peptide T1-SP10MN(A).
 XX
 KM V3; variable region; HIV; envelope peptide; gp120; T-helper; epitope;
 KM T-1.
 XX
 OS Synthetic.
 XX
 FH Key
 FT Region
 FT Location/Qualifiers
 XX 1.16
 XX /note= "printed in bold font"
 XX
 PN MO9414976-A1.
 XX
 PD 07-JUL-1994.
 XX
 PF 20-DEC-1993; 93MO-US012479.
 XX
 PR 18-DEC-1992; 92US-00992899.
 XX
 PA (UYDU-) UNIV DUKE.
 XX
 PI Pizzo SV, Chu CT, Oury TD;
 XX
 DR WPI; 1994-234708/28.
 XX
 PT Modifying immune responses to an antigen - by administering alpha-2-macro
 PT -globulin or a fragment capable of binding its receptor with the antigen.
 XX
 PS Disclosure; Page 40; 110pp; English.
 CC Synthetic T1-SP10 peptides are synthetic HIV peptides. They combine
 CC neutralising B-cell sites from the third variable region (V3) of the HIV
 CC envelope peptide gp120, with the gp120 T-helper epitope T-1. Several T1-
 CC AAs and T-cell responses in mice, goats and rhesus monkeys. T1-SP10MN(A)
 CC (MW 4771) can be complexed with alpha2-Macroglobulin (alpha2-M), or a C-
 CC terminal fragment thereof, either via the endogenous alpha2-M thioester
 CC or using a bifunctional crosslinker, such as the homo-bifunctional
 CC sulhydryl reactive crosslinker bis-moleimidodexane (ma) -
 CC treated alpha2-M. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 40 AA;

Query Match 95.1%; Score 202.5; DB 2; Length 40;
 Best Local Similarity 97.5%; Pred. No. 8.6e-18;
 Matches 39; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 KOIIMMOEVGKAMVA-TRPNYNNKRRRIHIGPRAFYTTK 39
 1 KOIIMMOEVGKAMVACTRPNNYNNKRRRIHIGPRAFYTTK 40

Db 1 KOIIMMOEVGKAMVACTRPNNYNNKRRRIHIGPRAFYTTK 40

RESULT 9

AAW16528
ID AAW16528 standard; peptide; 40 AA.
XX
AC AAW16528;
XX
XX 14-JAN-1998 (first entry)
DE Peptide (T1-SPI0(A)) comprising HIV antigenic determinant.
XX
XX Hydrophilic; antigenic determinant; HIV; envelope; glycoprotein; env; gp;
KW recognition; B lymphocyte; type specific; antibody; vaccine; protection;
KM immune response; infection; neutralisation.
XX
OS Human immunodeficiency virus.
XX
XX WO9714436-A1.
PN 24-APR-1997.
XX
XX 18-OCT-1996; 96WO-US016911.
PF 20-OCT-1995; 95US-00546515.
PR 09-FEB-1996; 96US-00599266.
XX
XX (UYDU-) UNIV DUKE.
PA
PI Haynes BF, Palker TJ;
XX
XX WPI; 1997-244862/22.
DR
XX
XX Synthetic human immunodeficiency virus vaccine - comprising hydrophilic
PT peptide corresponding to at least 1 antigenic determinant of envelope
PT glyco:protein recognised by B lymphocytes.
XX
XX Disclousure; Page 17; 104pp; English.
PS
XX
XX An essentially pure hydrophilic peptide, i.e. the present peptide,
CC comprising at least 1 antigenic determinant of human immunodeficiency
CC virus (HIV) envelope (env) glycoprotein (gp) recognised by B lymphocytes,
CC when covalently linked to a carrier molecule induces the production of
CC high titres of protective, type specific anti-HIV antibodies (Ab) in a
CC mammal. The peptide can be used in vaccines for producing a protective
CC immune response to HIV infection, while a HIV neutralising Ab can be
CC induced in a primate by administering a composition comprising HIV env
CC peptides that disrupt gp120/gp41 interactions
CC
SQ Sequence 40 AA;
Query Match 95.1%; Score 202.5; DB 2; Length 40;
Best Local Similarity 97.5%; Pred. No. 8.6e-18;
Matches 39; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 KOIINMGEVGRKMYA-TRPNYNKRRIHIGGRAFYTK 39
DB 1 KOIINMGEVGRKMYACTRPNYNKRRIHIGGRAFYTK 40
RESULT 10
AAW04025
ID AAW04025 standard; peptide; 40 AA.
XX
XX AAW04025;
AC
XX
XX 20-DEC-1999 (first entry)
DT
XX
XX HIV peptide T1-SPI0MN(A) for use in immunogenic complex.
DE
XX
XX Macroglobulin; HIV; immunogenic complex; human immunodeficiency virus;
KW hepatitis; antigen; vaccine.
XX
XX Human immunodeficiency virus.
OS
XX
XX WO9950303-A2.

XX
PD 07-OCT-1999.
XX
XX 01-APR-1999; 99WO-US007236.
PF
XX
XX 01-APR-1998; 98US-00053301.
PR 31-MAR-1999; 99US-00282826.
XX
XX (UYDU-) UNIV DUKE.
PA
PI Pizzo SV, Gron H;
XX
XX WPI; 1999-601324/51.
DR
XX
XX Immune response modulator alpha-2 macroglobulin complex useful in the
PT treatment of HIV or hepatitis.
PT
XX
XX Claim 3; Page 77; 103pp; English.
PS
XX
XX A stable complex comprising at least one intact biomolecule and activated
CC alpha-2-macroglobulin (alpha-2M) having an intact bait region is claimed,
CC in which the biomolecule is covalently bound to an amino acid residue of
CC a cleaved thiol ester of the alpha-2M; the amino acid residue being a
CC glutamyl residue and/or a cysteinyl residue. Preparation of the complex
CC comprises activation of alpha-2M with a nucleophilic compound followed by
CC incubation with the biomolecule at elevated temperature. Covalent
CC incorporation of the intact biomolecule is thus effected without use of a
CC protease. The obtained complex may be used as an antigen for stimulating
CC immune response, e.g. in the form of a vaccine. Enhanced presentation of
CC the biomolecule is provided, especially for those antigens which are
CC poorly immunogenic. Reduction of immunodominance of particular epitopes
CC is also provided. Preferably the biomolecule is an HIV antigen or a
CC hepatitis virus antigen, or a peptide, fragment, hybrid or chimeric
CC peptide thereof. The present sequence is a preferred example of an HIV
CC peptide which may be used in the complex
XX
SQ Sequence 40 AA;
Query Match 95.1%; Score 202.5; DB 2; Length 40;
Best Local Similarity 97.5%; Pred. No. 8.6e-18;
Matches 39; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 KOIINMGEVGRKMYA-TRPNYNKRRIHIGGRAFYTK 39
DB 1 KOIINMGEVGRKMYACTRPNYNKRRIHIGGRAFYTK 40
RESULT 11
AAE25518
ID AAE25518 standard; peptide; 40 AA.
XX
XX AAE25518;
AC
XX
XX 04-NOV-2002 (first entry)
DT
XX
XX Human immunodeficiency virus (HIV) T1-SPI0MN(A) peptide.
DE
XX
XX Stable complex; alpha-2-macroglobulin; immunocompetence; vaccine;
KW immune response; macroglobulin; tumour; human immunodeficiency virus; HIV;
KW cytostatic; antimicrobial; alpha2M; anti-HIV; virucide.
XX
XX Human immunodeficiency virus.
OS
XX
XX US6403092-B1.
PN
XX
XX 11-JUN-2002.
PD
XX
XX 31-MAR-1999; 99US-00282826.
PF
XX
XX 01-APR-1998; 98US-00053301.
PR
XX
XX (UYDU-) UNIV DUKE.
PA

PI Pizzo S, Gron H;
 XX
 DR WPI; 1999-601324/51.
 XX
 PT Immune response modulator alpha-2 macroglobulin complex useful in the
 XX treatment of HIV or hepatitis.
 XX
 PS Claim 3; Col 35; 34pp; English.

The invention relates to a stable complex comprising an intact
 CC biomolecule with a nucleophilic group which is covalently bound to
 CC activated alpha-2-macroglobulin (alpha2M) with an intact bait region.
 CC Stable complex is useful for enhancing host immunocompetence and for
 CC preparing vaccines for preventing and treating disease states. It is
 CC useful for increasing immune response to a poorly immunogenic antigen,
 CC and for suppressing immune response to a particularly antigen. It is
 CC in view of the existence on the macrophage of receptors for alpha2M. It
 CC is useful for treating cancer or infection, where the isolated protein is
 CC derived from tumour, abnormal cells or infectious organism, and this
 CC protein can be used as an antigen and prepared in alpha2M complex which
 CC is then administered in the form of vaccine to immunise mammalian
 CC patients in need of such treatment. It can also be used for inducing
 CC immune response against human immunodeficiency virus (HIV) antigens, and
 CC hepatitis virus antigens. The present sequence is HIV T1-SPI0M(A)
 CC peptide used in the exemplification of the invention

Query Match 95.1%; Score 202.5; DB 2; Length 40;
 Best Local Similarity 97.5%; Pred. No. 8.6e-18;
 Matches 39; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 KOIINMDEVGKAMYA-TRPNYKRRRIHIGRRAFYTTK 39
 1 KOIINMDEVGKAMYACTRPNYKRRRIHIGRRAFYTTK 40

Db
 RESULT 12
 ID AAY87621 standard; protein; 40 AA.
 XX
 AC AAY87621;
 XX
 DT 21-UTL-2000 (first entry)
 XX
 DE HIV SPI20 HD epitope.
 XX
 KW Immunogenic liposome; antigen; cytosolic; hydrophobic domain; epitope;
 XX vesicle forming lipid; immunization; vaccine; antimicrobial; SPI20.
 XX
 OS Human immunodeficiency virus.
 XX
 PN WO200016746-A2.
 XX
 PD 30-MAR-2000.
 XX
 PF 22-SEP-1999; 99WO-US020880.
 XX
 PR 22-SEP-1998; 98US-0101351P.
 XX
 FR 21-SEP-1999; 99US-0400723P.
 XX
 PA (MOLE-) MOLECULAR EXPRESS INC.
 XX
 PI Fujii G, Cramer DV, Ernst WA, Adler-Moore J, Perry LJ;
 XX
 DR WPI; 2000-283420/24.
 XX
 PT New immunogenic liposome composition for inducing an immunogenic response
 PT in a host animal against a variety of microbial agents and cancers,
 PT comprises vesicle forming lipid and an antigenic construct.
 XX
 XX Example II; Page 23; 44pp; English.

XX
 CC This invention describes a novel immunogenic liposome composition (C1)
 CC comprising vesicle forming lipids and an antigenic construct comprising
 CC one or more antigenic determinants and a hydrophobic domain (HD)
 CC associated with the membrane of the liposome composition. C1 is used to
 CC induce an immunogenic response in a host animal, preferably birds or
 CC mammals such as humans, against a variety of microbial agents and
 CC cancers. C1 provides effective and safe immunization. The epitopes can be
 CC readily changed to provide for maximal flexibility in vaccine design.
 CC Also, the expressed carrier protein is water soluble and can be easily
 CC purified using standard protein preparation methods. The products of the
 CC invention have antimicrobial and cytotoxic activity. This sequence of the
 CC method of the invention

Query Match 95.1%; Score 202.5; DB 3; Length 40;
 Best Local Similarity 97.5%; Pred. No. 8.6e-18;
 Matches 39; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 KOIINMDEVGKAMYA-TRPNYKRRRIHIGRRAFYTTK 39
 1 KOIINMDEVGKAMYACTRPNYKRRRIHIGRRAFYTTK 40

Db
 RESULT 13
 ID AAB49386 standard; peptide; 40 AA.
 XX
 AC AAB49386;
 XX
 DT 06-MAR-2001 (first entry)
 XX
 DE HIV peptide SEQ ID NO: 1.
 XX
 KW HIV; immunogenic peptide; immune response; monophosphoryl lipid A;
 XX antigen; infection; cancer; amyloid deposition.
 XX
 OS Human immunodeficiency virus.
 XX
 PN WO200069456-A2.
 XX
 PD 23-NOV-2000.
 XX
 PF 12-MAY-2000; 2000MO-US013156.
 XX
 FR 13-MAY-1999; 99US-0133963P.
 XX
 PA (AMCY) AMERICAN CYANAMID CO.
 XX
 PI Hagen M;
 XX
 DR WPI; 2001-024946/03.
 XX
 PT Antigenic composition having an antigen (e.g. viral protein) and an
 PT adjuvant, useful for enhancing humoral and cellular immune response in a
 PT host or as a prophylaxis against virus, bacterium, parasite, cancer cell
 PT or allergen.
 XX
 XX Claim 20; Page 109; 129pp; English.

The present invention provides an antigenic composition comprising an
 CC antigen with a 3-O-deacylated monophosphoryl lipid A or monophosphoryl
 CC lipid A adjuvant. The presence of the adjuvant causes an increased immune
 CC response. The antigen may be from a pathogenic bacterium, fungus, virus
 CC or parasite, a cancer cell, an allergen or from amyloid peptide protein.
 CC The composition can be used in the prevention and treatment of infection,
 CC cancer and diseases caused by amyloid deposition. It is particularly
 CC useful against HIV, Neisseria gonorrhoeae and respiratory syncytial virus
 XX
 SO Sequence 40 AA;

Query Match 95.1%; Score 202.5; DB 4; Length 40;
Best Local Similarity 97.5%; Pred. No. 8.6e-18;
Matches 39; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 KOIINMGEVGKAMYA-TRPNYKRRKRIHIGPRAFYTTK 39
1 KOIINMGEVGKAMYACTRPNYKRRKRIHIGPRAFYTTK 40

DB

RESULT 14
AAE26075 standard; peptide; 40 AA.

AC AAE26075;
XX
XX 29-AUG-2003 (revised)
DT 14-NOV-2002 (first entry)
XX
XX Human immunodeficiency virus type 1 (HIV-1) peptide, TISPL0MN (A) (+Cys).

DE Antigenic composition; cancer; aminoalkyl glucosamine phosphate compound;
KM AGP; immune response; cytotoxic T lymphocyte; allergic response; tumour;
KM amyloid deposition; vaccine; antifungal; antibacterial; antiparasitic;
KM cytostatic; immunostimulant; virucide; HIV-1 peptide.

XX Human immunodeficiency virus 1.
OS WO200238177-A2.
XX
XX 16-MAY-2002.
PD 08-NOV-2001; 2001MO-US046943.
XX
XX 10-NOV-2000; 2000US-0247100P.
PR 18-OCT-2001; 2001US-0330345P.
XX
XX (AMCY) AMERICAN CYANAMID CO.
PA
XX Hagen M;
XX
XX WPI; 2002-636409/68.
DR
XX
XX Antigenic composition for use in enhancing immune response of antigen,
PT has selected antigen, and combination of adjuvant comprising an
PT aminoalkyl glucosamine phosphate compound, and cytokine or lymphokine.

PS Claim 14; Page 71; 94pp; English.

XX The invention relates to an antigenic composition comprising a selected
XX antigen from a pathogenic virus, bacterium, fungus or parasite, or from a
XX cancer or tumour cell, or from an allergen, or from a self molecule, and
XX an combination of adjuvant comprising an aminoalkyl glucosamine phosphate
XX compound (AGP), or its derivative or analogue, and a cytokine or
XX lymphokine, or an agonist to it. The invention is useful for increasing
XX the ability of an antigenic composition (enhancing immune response)
XX containing a selected antigen from a pathogenic virus, bacterium, fungus
XX or parasite to elicit an immune response especially cytotoxic T
XX lymphocytes; a selected antigen a cancer or tumour cell to elicit
XX therapeutic or prophylactic anti-cancer effect; a selected allergen to
XX moderate an allergic response; or a selected antigen from a molecule or
XX its portion representing those produced by a host in an undesired manner,
XX amount or location so as to reduce an undesired effect. in a vertebrate
XX host. The invention is useful for increasing the ability of an antigenic
XX composition to prevent or treat disease characterised by amyloid
XX deposition in a vertebrate host. The invention is useful as a vaccine.
XX The present sequence is HIV-1 peptide, TISPL0MN (A) (+Cys). (Updated on
XX 29-AUG-2003 to standardise OS field)

SO Sequence 40 AA;

Query Match 95.1%; Score 202.5; DB 5; Length 40;
Best Local Similarity 97.5%; Pred. No. 8.6e-18;
Matches 39; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 KOIINMGEVGKAMYA-TRPNYKRRKRIHIGPRAFYTTK 39
1 KOIINMGEVGKAMYACTRPNYKRRKRIHIGPRAFYTTK 40

DB

RESULT 15
ABO01836 standard; peptide; 40 AA.

ID ABO01836;
XX
XX 23-OCT-2003 (revised)
DT 07-AUG-2003 (first entry)
XX
XX HIV MN envelope region peptide T1-SPI0MN (A).

DE HIV; gp41; envelope protein; fusion protein; toleragen; immunomodulatory;
XX T cell response; B cell response; immune tolerance; TSH; AIDS;
XX acetylcholine receptor; insulin protein; myelin basic protein;
XX thyroid stimulating hormone receptor; autoimmune T cell antigen;
XX retinal S protein; autoimmune disease; myasthenia gravis;
XX diabetes mellitus; autoimmune thyroid disease; Grave's disease;
XX experimental autoimmune encephalomyelitis; multiple sclerosis;
XX autoimmune retinouveitis; Bechet's syndrome; idiopathic retinouveitis;
XX HTLV-1 associated myelopathy; tropical spastic paraparesis;
XX acquired immunodeficiency syndrome.

XX Human immunodeficiency virus 1; strain MN.
OS US2003022826-A1.
XX
XX 30-JAN-2003.
PD 21-SEP-2001; 2001US-00956940.
XX
XX 08-SEP-1987; 87US-00093854.
PR 01-OCT-1990; 90US-00591109.
PR 10-FEB-1992; 92US-00833429.
PR 10-FEB-1993; 93US-00015987.
PR 02-JUN-1995; 95US-00460673.
PR 11-AUG-2000; 2000US-00635845.
XX
XX (UYDU-) UNIV DUKE.
PA
XX Haynes BF;
XX
XX WPI; 2003-456303/43.
DR
XX
XX Inducing immune tolerance in a mammal to an immunogenic peptide or
PT protein, by administering to the mammal a synthetic immune system
PT toleragen comprising a hydrophobic peptide linked to the peptide or
PT protein.

PS Disclosure; Fig 10; 27pp; English.

XX The invention relates to inducing immune tolerance in a mammal to an
XX immunogenic peptide or protein, involving administering to the mammal a
XX synthetic immune system toleragen comprising 2-20 amino acid hydrophobic
XX peptide (especially the HIV envelope gp41 fusion protein (F) peptide
XX appearing as ABO01846) linked to the N-terminus or C-terminus of the
XX immunogenic peptide or protein, under conditions such that the immune
XX tolerance is induced. The method is useful for inducing immune tolerance
XX in a mammal to an immunogenic peptide or protein such as an acetylcholine
XX receptor protein, an insulin protein, a thyroid stimulating hormone (TSH)
XX receptor protein, myelin basic protein, an autoimmune T cell antigen, and
XX a retinal S protein, or their fragments and thus may be used to treat
XX autoimmune diseases such as myasthenia gravis, diabetes mellitus,
XX autoimmune thyroid disease (e.g Grave's disease), experimental autoimmune
XX encephalomyelitis, multiple sclerosis, autoimmune retinouveitis, Bechet's
XX syndrome, idiopathic retinouveitis, HTLV-1 associated myelopathy,
XX tropical spastic paraparesis and acquired immunodeficiency syndrome
XX (AIDS). The mammal is a primate, preferably human. The present sequence

CC represents a region of an HIV strain envelope glycoprotein suitable for
 CC testing as the hydrophobic peptide region of the toleragen. (Updated on
 XX 23-Oct-2003 to standardise OS field)
 SQ Sequence 40 AA;

Query Match 95.1%; Score 202.5; DB 7; Length 40;
 Best Local Similarity 97.5%; Pred. No. 8.6e-18;
 Matches 39; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
 QY 1 KOIIMMOEVGKAWYA-TREPNYKRRKRIHIGGRAFYTTK 39
 Db 1 KOIIMMOEVGKAWYACTREPNYKRRKRIHIGGRAFYTTK 40

Search completed: February 24, 2005, 07:27:39
 Job time : 71 secs

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OM protein - protein search, using sw model

Run on: February 24, 2005, 07:26:48 ; Search time 43 Seconds
(without alignments)
67.705 Million cell updates/sec

Title: US-10-009-473-2
Perfect score: 213
Sequence: 1 KOIIMMOEVGKAMYATRPYNKRRKRIHIGRAFYTTK 39

Scoring table:
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Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	202.5	95.1	40	4 US-09-282-826-1	Sequence 1, Appl
2	202.5	95.1	40	5 PCT-US93-12479-2	Sequence 2, Appl
3	194.5	91.3	40	1 US-08-257-528B-21	Sequence 21, Appl
4	194.5	91.3	40	1 US-08-460-602A-21	Sequence 21, Appl
5	194.5	91.3	40	1 US-08-463-966A-21	Sequence 21, Appl
6	194.5	91.3	40	1 US-08-465-217A-21	Sequence 21, Appl
7	194.5	91.3	40	2 US-08-464-329A-21	Sequence 21, Appl
8	194.5	91.3	40	2 US-08-462-507A-21	Sequence 21, Appl
9	194.5	91.3	40	2 US-08-467-881A-21	Sequence 21, Appl
10	162.5	76.3	35	1 US-08-257-528B-23	Sequence 23, Appl
11	162.5	76.3	35	1 US-08-460-602A-23	Sequence 23, Appl
12	162.5	76.3	35	1 US-08-463-966A-23	Sequence 23, Appl
13	162.5	76.3	35	1 US-08-465-217A-23	Sequence 23, Appl
14	162.5	76.3	35	2 US-08-464-329A-23	Sequence 23, Appl
15	162.5	76.3	35	2 US-08-462-507A-23	Sequence 23, Appl
16	162.5	76.3	35	2 US-08-467-881A-23	Sequence 23, Appl
17	152.5	71.6	39	2 US-08-455-625-28	Sequence 28, Appl
18	152.5	71.6	39	3 US-08-455-685-28	Sequence 28, Appl
19	152.5	71.6	39	3 US-08-060-988A-28	Sequence 28, Appl
20	152.5	71.6	39	4 US-09-508-552-9	Sequence 9, Appl
21	152.5	71.6	39	5 PCT-US94-05142-28	Sequence 28, Appl
22	145	68.1	45	1 US-08-257-528B-89	Sequence 89, Appl
23	145	68.1	45	1 US-08-460-602A-89	Sequence 89, Appl
24	145	68.1	45	1 US-08-463-966A-89	Sequence 89, Appl
25	145	68.1	45	1 US-08-465-217A-89	Sequence 89, Appl
26	145	68.1	45	2 US-08-464-329A-89	Sequence 89, Appl
27	145	68.1	45	2 US-08-462-507A-89	Sequence 89, Appl

28	145	68.1	45	2 US-08-467-881A-89	Sequence 89, Appl
29	144.5	67.8	41	4 US-09-282-826-2	Sequence 2, Appl
30	139.5	65.5	41	1 US-08-257-528B-46	Sequence 46, Appl
31	139.5	65.5	41	1 US-08-460-602A-46	Sequence 46, Appl
32	139.5	65.5	41	1 US-08-463-966A-46	Sequence 46, Appl
33	139.5	65.5	41	1 US-08-465-217A-46	Sequence 46, Appl
34	139.5	65.5	41	2 US-08-464-329A-46	Sequence 46, Appl
35	139.5	65.5	41	2 US-08-462-507A-46	Sequence 46, Appl
36	139.5	65.5	41	2 US-08-467-881A-46	Sequence 46, Appl
37	135.5	63.6	34	1 US-08-257-528B-45	Sequence 45, Appl
38	135.5	63.6	34	1 US-08-460-602A-45	Sequence 45, Appl
39	135.5	63.6	34	1 US-08-463-966A-45	Sequence 45, Appl
40	135.5	63.6	34	1 US-08-465-217A-45	Sequence 45, Appl
41	135.5	63.6	34	2 US-08-464-329A-45	Sequence 45, Appl
42	135.5	63.6	34	2 US-08-462-507A-45	Sequence 45, Appl
43	135.5	63.6	34	2 US-08-467-881A-45	Sequence 45, Appl
44	128	60.1	24	1 US-08-257-528B-20	Sequence 20, Appl
45	128	60.1	24	1 US-08-460-602A-20	Sequence 20, Appl

ALIGNMENTS

```

RESULT 1
US-09-282-826-1
; Sequence 1, Application US/09282826A
; Patent No. 6403092
; GENERAL INFORMATION:
; APPLICANT: Pizzo, Salvatore
; APPLICANT: Gron, Hanne
; TITLE OF INVENTION: IMMUNE RESPONSE MODULATOR ALPHA-2 MACROGLOBULIN COMPLEX
; FILE REFERENCE: 2295-1-001CIP
; CURRENT APPLICATION NUMBER: US/09/282, 826A
; EARLIER APPLICATION NUMBER: 09/053, 301
; EARLIER FILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 40
; TYPE: PRT
; ORGANISM: HTV
US-09-282-826-1

Query Match          95.1%; Score 202.5; DB 4; Length 40;
Best Local Similarity 97.5%; Pred. No. 1.6e-22;
Matches 39; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY      1 KOIIMMOEVGKAMYA-TRPNYKRRKRIHIGRAFYTTK 39
Db      1 KOIIMMOEVGKAMYACTRPYNKRRKRIHIGRAFYTTK 40

RESULT 2
PCT-US93-12479-2
; Sequence 2, Application PC/TUS9312479
; GENERAL INFORMATION:
; APPLICANT: Duke University, (except for the U.S.)
; APPLICANT: Pizzo, Salvatore V.
; APPLICANT: Chu, Charleen T.
; APPLICANT: Oury, Timothy D.
; TITLE OF INVENTION: IMMUNE RESPONSE MODULATOR COMPLEX, AND
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSER: David A. Jackson, Esq.
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/12479
FILING DATE: 20-DEC-1993
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/992,899
FILING DATE: 18-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 931-1-008 PCT/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 487-5800
TELEFAX: (201) 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
PUBLICATION INFORMATION:
AUTHORS: Hart, Mary K.
AUTHORS: Weinhold, Kent J.
AUTHORS: Scaerle, Richard M.
AUTHORS: Washburn, Eileen M.
AUTHORS: Clark, Cynthia A.
AUTHORS: Palmer, Thomas J.
AUTHORS: Haynes, Barton F.
TITLE: Priming of anti-human immunodeficiency virus
TITLE: carrier-free HIV synthetic peptides
JOURNAL: Proc. Natl. Acad. Sci. U.S.A.
VOLUME: 88
PAGES: 9448-9452
DATE: November-1991
RELEVANT RESIDUES IN SEQ ID NO: 2: FROM 1 TO 40
PCT-US93-12479-2

Query Match
Best Local Similarity 95.1%; Score 202.5; DB 5; Length 40;
Matches 39; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Oy
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Db
1 KOIINMGEVGRKAWYACTRPYNNKRRKRIHIGGRAFYTTK 40

RESULT 3
US-08-257-5288-21
Sequence 21, Application US/08257528B
Patent No. 5639854
GENERAL INFORMATION:
APPLICANT: SIA, Charles D.Y.
APPLICANT: CHONG, Pele
TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSER: SIm & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/257,528B
FILING DATE: 09-JUN-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, MICHAEL I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-336 MIS:jfb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1163
TELEFAX: (416) 595-1155
US-08-257-5288-21

Query Match
Best Local Similarity 91.3%; Score 194.5; DB 1; Length 40;
Matches 38; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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Db
1 KOIINMGEVGRKAWYACTRPYNNKRRKRIHIGGRAFYTTK 40

RESULT 4
US-08-460-602A-21
Sequence 21, Application US/08460602A
Patent No. 5759769
GENERAL INFORMATION:
APPLICANT: SIA, Charles D.Y.
APPLICANT: CHONG, Pele
TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSER: SIm & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,602A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257,528
FILING DATE: 09-JUN-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/073,378
FILING DATE: 09-JUN-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, MICHAEL I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-450 MIS:jfb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163

```

INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-460-602A-21

Query Match 91.3%; Score 194.5; DB 1; Length 40;
Best Local Similarity 95.0%; Pred. No. 2.4e-21;
Matches 38; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 1 KOIIMMOEVEKAMYA-TRPNYKRRRIHIGRAFYTTK 39
Db 1 KOIIMMOEVEKAMYACTRPNYKRRRIHIGRAFYTTK 40

RESULT 5

US-08-463-966A-21
Sequence 21, Application US/08463966A
Patent No. 5795955

GENERAL INFORMATION:
APPLICANT: SIA, Charles D. Y.
APPLICANT: CHONG, Pele
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada

ZIP: M5G 1R7

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,966A

FILING DATE: 05-JUN-1995

CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257,528

FILING DATE: 09-JUN-1994

CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/073,378

FILING DATE: 09-JUN-1993

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: STEWART, MICHAEL I.

REGISTRATION NUMBER: 24,973

REFERENCE/DOCKET NUMBER: 1038-487 MIS:j.b

TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155

TELEFAX: (416) 595-1163

INFORMATION FOR SEQ ID NO: 21:

SEQUENCE CHARACTERISTICS:

LENGTH: 40 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear
US-08-463-966A-21

Query Match 91.3%; Score 194.5; DB 1; Length 40;
Best Local Similarity 95.0%; Pred. No. 2.4e-21;
Matches 38; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 1 KOIIMMOEVEKAMYA-TRPNYKRRRIHIGRAFYTTK 39
Db 1 KOIIMMOEVEKAMYACTRPNYKRRRIHIGRAFYTTK 40

RESULT 6

US-08-465-217A-21
Sequence 21, Application US/08465217A
Patent No. 5800822

GENERAL INFORMATION:
APPLICANT: SIA, Charles D. Y.
APPLICANT: CHONG, Pele
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada

ZIP: M5G 1R7

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,217A

FILING DATE: 05-JUN-1995

CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257,528

FILING DATE: 09-JUN-1994

CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/073,378

FILING DATE: 09-JUN-1993

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: STEWART, MICHAEL I.

REGISTRATION NUMBER: 24,973

REFERENCE/DOCKET NUMBER: 1038-486 MIS:j.b

TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155

TELEFAX: (416) 595-1163

INFORMATION FOR SEQ ID NO: 21:

SEQUENCE CHARACTERISTICS:

LENGTH: 40 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear
US-08-465-217A-21

Query Match 91.3%; Score 194.5; DB 1; Length 40;
Best Local Similarity 95.0%; Pred. No. 2.4e-21;
Matches 38; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 1 KOIIMMOEVEKAMYA-TRPNYKRRRIHIGRAFYTTK 39
Db 1 KOIIMMOEVEKAMYACTRPNYKRRRIHIGRAFYTTK 40

RESULT 7

US-08-464-329A-21
Sequence 21, Application US/08464329A
Patent No. 5817754

GENERAL INFORMATION:

APPLICANT: SIA, Charles D. Y.

APPLICANT: CHONG, Pele

APPLICANT: KLEIN, Michel H.

TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides

NUMBER OF SEQUENCES: 101

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue

CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,329A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257,528
FILING DATE: 09-JUN-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/073,378
FILING DATE: 09-JUN-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, MICHAEL I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-449 MIS:jb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1155
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-464-329A-21

Query Match
Best Local Similarity 91.3%; Score 194.5; DB 2; Length 40;
Matches 38; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 1 KOIIMMOEVKAMYA-TRPNYKRRKHIGRAFYTTK 39
Db 1 KOIIMMOEVKAMYACTRPNYKRRKHIGRAFYTTK 40

RESULT 8
US-08-462-507A-21
Sequence 21, Application US/08462507A
Patent No. 5876731
GENERAL INFORMATION:
APPLICANT: SIA, Charles D.Y.
APPLICANT: CHONG, Pele
TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,507A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257,528

FILING DATE: 09-JUN-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/073,378
FILING DATE: 09-JUN-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, MICHAEL I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-451 MIS:jb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1155
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-462-507A-21

Query Match
Best Local Similarity 91.3%; Score 194.5; DB 2; Length 40;
Matches 38; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 1 KOIIMMOEVKAMYA-TRPNYKRRKHIGRAFYTTK 39
Db 1 KOIIMMOEVKAMYACTRPNYKRRKHIGRAFYTTK 40

RESULT 9
US-08-467-881A-21
Sequence 21, Application US/08467881A
Patent No. 5951986
GENERAL INFORMATION:
APPLICANT: SIA, Charles D.Y.
APPLICANT: CHONG, Pele
TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,881A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257,528
FILING DATE: 09-JUN-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/073,378
FILING DATE: 09-JUN-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, MICHAEL I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-488 MIS:jb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1155
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:

LENGTH: 40 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-467-881A-21

Query Match 91.3%; Score 194.5; DB 2; Length 40;
Best Local Similarity 95.0%; Pred. No. 2.4e-21;
Matches 38; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 1 KOIIMMOEVGKAMYA-TRPNYKRRRIHIGPRAFYTTK 39
Db 1 KOIIMMOEVGKAMYA-TRPNYKRRRIHIGPRAFYTTK 40

RESULT 10
US-08-257-528B-23

Sequence 23, Application US/08257528B
Patent No. 5639854
GENERAL INFORMATION:
APPLICANT: SIA, Charles D. Y.
APPLICANT: CHONG, Pele
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7

COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/257, 528B
FILING DATE: 09-JUN-1994
CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:
NAME: STEWART, MICHAEL I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-336 MIS-Jb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163

INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-257-528B-23

Query Match 76.3%; Score 162.5; DB 1; Length 35;
Best Local Similarity 84.6%; Pred. No. 9.6e-17;
Matches 33; Conservative 0; Mismatches 1; Indels 5; Gaps 1;

Qy 1 KOIIMMOEVGKAMYA-TRPNYKRRRIHIGPRAFYTTK 39
Db 1 KOIIMMOEVGKAMYA-TRPNYKRRRIHIGPRAFYTTK 34

RESULT 11
US-08-460-602A-23

Sequence 23, Application US/08460602A
Patent No. 5759769
GENERAL INFORMATION:
APPLICANT: SIA, Charles D. Y.
APPLICANT: CHONG, Pele
APPLICANT: KLEIN, Michel H.

TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460, 602A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257, 528
FILING DATE: 09-JUN-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/073, 378
FILING DATE: 09-JUN-1993

ATTORNEY/AGENT INFORMATION:
NAME: STEWART, MICHAEL I.

REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-450 MIS-Jb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163

INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-460-602A-23

Query Match 76.3%; Score 162.5; DB 1; Length 35;
Best Local Similarity 84.6%; Pred. No. 9.6e-17;
Matches 33; Conservative 0; Mismatches 1; Indels 5; Gaps 1;

Qy 1 KOIIMMOEVGKAMYA-TRPNYKRRRIHIGPRAFYTTK 39
Db 1 KOIIMMOEVGKAMYA-TRPNYKRRRIHIGPRAFYTTK 34

RESULT 12
US-08-463-966A-23

Sequence 23, Application US/08463966A
Patent No. 5795955
GENERAL INFORMATION:

APPLICANT: SIA, Charles D. Y.
APPLICANT: CHONG, Pele
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/463,966A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257,528
FILING DATE: 09-JUN-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/073,378
FILING DATE: 09-JUN-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, MICHAEL I.
REGISTRATION NUMBER: 24,973
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1153
TELEFAX: (416) 595-1155
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-463-966A-23

Query Match
Best Local Similarity 76.3%; Score 162.5; DB 1; Length 35;
Matches 33; Conservative 0; Mismatches 1; Indels 5; Gaps 1;

QY 1 KOIIMMGEVGRKMYATRRNPKRKHIGPGRAFYTTK 39
DB 1 KOIIMMGEVGRKMYA-----NKKRIHIGPGRAFYTTK 34

RESULT 13
US-08-465-217A-23
Sequence 23; Application US/08465217A
Patent No. 5800822
GENERAL INFORMATION:
APPLICANT: SIA, Charles D.Y.
APPLICANT: CHONG, Pele
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSER: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,217A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257,528
FILING DATE: 09-JUN-1994
CLASSIFICATION: 424
APPLICATION DATA:
FILING DATE: 08/073,378
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, MICHAEL I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-486 MIS:jdb

TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1153
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-465-217A-23

Query Match
Best Local Similarity 76.3%; Score 162.5; DB 1; Length 35;
Matches 33; Conservative 0; Mismatches 1; Indels 5; Gaps 1;

QY 1 KOIIMMGEVGRKMYATRRNPKRKHIGPGRAFYTTK 39
DB 1 KOIIMMGEVGRKMYA-----NKKRIHIGPGRAFYTTK 34

RESULT 14
US-08-464-329A-23
Sequence 23; Application US/08464329A
Patent No. 5817754
GENERAL INFORMATION:
APPLICANT: SIA, Charles D.Y.
APPLICANT: CHONG, Pele
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSER: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,329A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257,528
FILING DATE: 09-JUN-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/073,378
FILING DATE: 09-JUN-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, MICHAEL I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-449 MIS:jdb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1153
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-464-329A-23

Query Match
Best Local Similarity 76.3%; Score 162.5; DB 2; Length 35;
Matches 33; Conservative 0; Mismatches 1; Indels 5; Gaps 1;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 24, 2005, 07:23:23 ; Search time 177 Seconds
(without alignments)
112.831 Million cell updates/sec

Title: US-10-009-473-2

Perfect score: 213

Sequence: 1 KQIIMMQBVGKAMYATRPNNKRIHIGGRAFYTTK 39

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	128	60.1	205	2	090007 human immun
2	128	60.1	856	1	P05877 human immun
3	128	60.1	857	2	090296 human immun
4	128	60.1	857	2	Q6B002 human immun
5	128	60.1	857	2	Q9YU15 human immun
6	128	60.1	861	2	090295 human immun
7	119	55.9	861	2	090294 human immun
8	113	53.1	162	2	091191 human immun
9	111	52.1	108	2	09YR94 human immun
10	110	51.6	63	2	Q85831 human immun
11	110	51.6	63	2	Q85837 human immun
12	110	51.6	70	2	Q70454 human immun
13	110	51.6	70	2	Q70457 human immun
14	110	51.6	73	2	093001 human immun
15	109.5	51.4	136	2	Q9WMD3 human immun
16	109.5	51.4	136	2	Q9WMD4 human immun
17	109	51.2	71	2	Q6IRU2 human immun
18	109	51.2	71	2	Q6IRU4 human immun
19	109	51.2	71	2	Q6IRU7 human immun
20	109	51.2	94	2	097196 human immun
21	109	51.2	100	2	Q91DT4 human immun
22	109	51.2	207	2	Q8QDA3 human immun
23	109	51.2	212	2	Q75073 human immun
24	109	51.2	213	2	Q75066 human immun
25	109	51.2	213	2	Q75072 human immun
26	109	51.2	215	2	Q75070 human immun
27	108	50.7	35	2	Q78813 human immun
28	108	50.7	73	2	Q72417 human immun
29	108	50.7	92	2	Q70063 human immun
30	108	50.7	93	2	Q80328 human immun
31	108	50.7	93	2	Q80329 human immun

32	108	50.7	93	2	Q80330 human immun
33	108	50.7	93	2	Q80331 human immun
34	108	50.7	93	2	Q80333 human immun
35	108	50.7	104	2	Q904X4 human immun
36	108	50.7	857	2	Q92821 human immun
37	108	50.7	857	2	Q92822 human immun
38	108	50.7	857	2	Q92823 human immun
39	108	50.7	857	2	Q71013 human immun
40	108	50.7	857	2	Q89654 human immun
41	106.5	50.0	203	2	Q9QED4 human immun
42	106.5	50.0	205	2	Q9QDR5 human immun
43	106.5	50.0	205	2	Q9QDR8 human immun
44	106.5	50.0	205	2	Q9QDR9 human immun
45	106.5	50.0	205	2	Q9QDS0 human immun

ALIGNMENTS

```

RESULT 1
090007 PRELIMINARY; PRT; 205 AA.
ID 090007
AC 090007;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name-env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxId=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98248614; PubMed=9582120; DOI=10.1126/science.280.5366.1073;
RA Frenkel L.W., Mullins J.I., Learn G.H., Manns-Arcuno L.,
RA Herring B.L., Kallish M.L., Steketee R.W., Thea D.M., Nichols J.E.,
RA Liu S.-L., Harmache A., He X., Muthui D., Madan A., Hood L.,
RA Haase A.T., Zupanic M., Staekus K., Wolinsky S.W., Krogstad P.,
RA Zhao J.-Q., Chen I., Kouy R., Ho D.D., Korber B.T., Apple R.J.,
RA Coombs R.W., Pahwa S., Roberts N.J. Jr.;
RT "Genetic evaluation of suspected cases of transient HIV-1 infection of
RT infants."
RT Science 280:1073-1077 (1998).
RL EMBL; AF065539; AAC21502.1; -.
DR HSP; P05877; IN10.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; C:structural molecule activity; IEA.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 205
SQ SEQUENCE 205 AA; 23153 MW; D0B957326F130724 CRC64;

Query Match 60.1%; Score 128; DB 2; Length 205;
Best Local Similarity 100.0%; Pred. No. 3.5e-10;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 TRPNYKRRKRIHIGGRAFYTTK 39
Db 31 TRPNYKRRKRIHIGGRAFYTTK 53

RESULT 2
ENV_HVLMN STANDARD; PRT; 856 AA.
ID ENV_HVLMN
AC P05877;
DT 01-NOV-1988 (rel. 09, Created)
DT 01-NOV-1988 (rel. 09, Last sequence update)
DT 25-OCT-2004 (rel. 45, Last annotation update)
DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane

```

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FT CARBOHYD 612 612 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 617 617 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 626 626 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 638 638 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 816 816 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 856 AA; 97140 MW; D197D80940BE8732 CRC64;

Query Match
Best Local Similarity 100.0%; Score 128; DB 1; Length 856;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 TRPNYNRKRRIHIGPERAFYTTK 39
DB 302 TRPNYNRKRRIHIGPERAFYTTK 324

RESULT 3
O90296 PRELIMINARY; PRT; 857 AA.
AC O90296;
DT 01-NOV-1998 (TREMBLrel. 08 Created)
DT 01-NOV-1998 (TREMBLrel. 08 Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 28, Last annotation update)
DE Envelope glycoprotein.
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OC NCBI_TaxId=11676;
RN [1]
RP SEQUENCE FROM N.A.

RX MEDLINE=98362112; PubMed=9696803;
RA Park E.J., Vajic L.K., Anand R., Theodore T.S., Quinan G.V. Jr.;
RT "Mutations in both gp120 and gp41 are responsible for the broad
RT neutralization resistance of variant human immunodeficiency virus type
RL J. Virol. 72:7089-7107(1998).
DR EMBL: AF075721; AAC31818.1; -.
DR HSSP: P05877; INDO.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0019028; C:viral capsid; IEA.
DR GO: GO:0019031; C:viral envelope; IEA.
DR GO: GO:0005198; F:structural molecule activity; IEA.
DR InterPro: IPR000328; Env GP41.
DR Pfam: PF00516; GP120.1.
DR Pfam: PF00517; GP120.1.
DR AIDS; Coat protein; Envelope protein; Glycoprotein; Polyprotein;
KW Transmembrane.
SQ SEQUENCE 857 AA; 97064 MW; E0D8599CC50C6F4 CRC64;

Query Match
Best Local Similarity 100.0%; Score 128; DB 2; Length 857;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 TRPNYNRKRRIHIGPERAFYTTK 39
DB 302 TRPNYNRKRRIHIGPERAFYTTK 324

RESULT 4
O6BC02 PRELIMINARY; PRT; 857 AA.
AC O6BC02;
DT 25-OCT-2004 (TREMBLrel. 28 Created)
DT 25-OCT-2004 (TREMBLrel. 28 Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OC NCBI_TaxId=11676;
RN [1]
RP SEQUENCE FROM N.A.

```

RA Binley J.M., Wrin T., Zwick M.B., Korber B., Wang M., Chappey C.,
 RA Stiegler G., Kunert R., Zolla-Pazner S., Katinger H.,
 RA Petropoulos C.J., Burton D.R.; The cross-clade neutralizing activity of a
 RT "Comprehensive analysis of the cross-clade neutralizing activity of a
 RT panel of anti-HIV-1 monoclonal antibodies.";
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY669737; AAT67509.1; -
 DR GO; GO:0019031; C:Viral envelope; IEA.
 DR GO; GO:0005198; F:Structural molecule activity; IEA.
 DR InterPro; IPR000328; Env_Gp41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 KW AIDS; Coat protein; Envelope protein; Glycoprotein; Polypeptide;
 KW Transmembrane.
 FT NON_TER
 PT 857
 SQ SEQUENCE 857 AA; 97206 MW; 4ED03F3D85C91205 CRC64;

Query Match 60.1%; Score 128; DB 2; Length 857;
 Best Local Similarity 100.0%; Pred. No. 1.8e-09;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 TRPNYKRRKRIHIGPRAFYTTK 39
 Db 302 TRPNYKRRKRIHIGPRAFYTTK 324

RESULT 5
 Q9YUL5 PRELIMINARY; PRT; 857 AA.

AC Q9YUL5;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Envelope glycoprotein.
 GN Name=env;
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OC NCBI_TaxID=11676;
 RN (1)
 RP SEQUENCE FROM N.A.

RX MEDLINE=98362112; PubMed=9696803;
 RA Park E.J., Vujcic L.K., Anand R., Theodore T.S., Quinan G.V. Jr.;
 RT "Mutations in both gp120 and gp41 are responsible for the broad
 RT neutralization resistance of variant human immunodeficiency virus type
 RT 1 MN to antibodies directed at V3 and non-V3 epitopes.";
 RL J. Virol. 72:7099-7107(1998).
 DR EMBL; AF075722; AAC31819.1; -
 DR HSSP; P05877; 1N70.
 DR GO; GO:0016021; C:Integral to membrane; IEA.
 DR GO; GO:0019028; C:Viral capsid; IEA.
 DR GO; GO:0019031; C:Viral envelope; IEA.
 DR GO; GO:0005198; F:Structural molecule activity; IEA.
 DR InterPro; IPR000328; Env_Gp41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 KW AIDS; Coat protein; Envelope protein; Glycoprotein; Polypeptide;
 KW Transmembrane.
 SQ SEQUENCE 857 AA; 97095 MW; 922D362810C60DA8 CRC64;

Query Match 60.1%; Score 128; DB 2; Length 857;
 Best Local Similarity 100.0%; Pred. No. 1.8e-09;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 TRPNYKRRKRIHIGPRAFYTTK 39
 Db 302 TRPNYKRRKRIHIGPRAFYTTK 324

RESULT 6
 Q90295 PRELIMINARY; PRT; 861 AA.

AC Q90295;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Envelope glycoprotein.
 GN Name=env;
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OC NCBI_TaxID=11676;
 RN (1)
 RP SEQUENCE FROM N.A.

RX MEDLINE=98362112; PubMed=9696803;
 RA Park E.J., Vujcic L.K., Anand R., Theodore T.S., Quinan G.V. Jr.;
 RT "Mutations in both gp120 and gp41 are responsible for the broad
 RT neutralization resistance of variant human immunodeficiency virus type
 RT 1 MN to antibodies directed at V3 and non-V3 epitopes.";
 RL J. Virol. 72:7099-7107(1998).
 DR EMBL; AF075720; AAC31817.1; -
 DR HSSP; P05877; 1N70.
 DR GO; GO:0016021; C:Integral to membrane; IEA.
 DR GO; GO:0019028; C:Viral capsid; IEA.
 DR GO; GO:0019031; C:Viral envelope; IEA.
 DR GO; GO:0005198; F:Structural molecule activity; IEA.
 DR InterPro; IPR000328; Env_Gp41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 KW AIDS; Coat protein; Envelope protein; Glycoprotein; Polypeptide;
 KW Transmembrane.
 SQ SEQUENCE 861 AA; 97616 MW; 36593D08429DC700 CRC64;

Query Match 60.1%; Score 128; DB 2; Length 861;
 Best Local Similarity 100.0%; Pred. No. 1.8e-09;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 TRPNYKRRKRIHIGPRAFYTTK 39
 Db 302 TRPNYKRRKRIHIGPRAFYTTK 324

RESULT 7
 Q90294 PRELIMINARY; PRT; 861 AA.
 AC Q90294;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Envelope glycoprotein.
 GN Name=env;
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OC NCBI_TaxID=11676;
 RN (1)
 RP SEQUENCE FROM N.A.

RX MEDLINE=98362112; PubMed=9696803;
 RA Park E.J., Vujcic L.K., Anand R., Theodore T.S., Quinan G.V. Jr.;
 RT "Mutations in both gp120 and gp41 are responsible for the broad
 RT neutralization resistance of variant human immunodeficiency virus type
 RT 1 MN to antibodies directed at V3 and non-V3 epitopes.";
 RL J. Virol. 72:7099-7107(1998).
 DR EMBL; AF075719; AAC33788.1; -
 DR HSSP; P05877; 1N70.
 DR GO; GO:0016021; C:Integral to membrane; IEA.
 DR GO; GO:0019028; C:Viral capsid; IEA.
 DR GO; GO:0019031; C:Viral envelope; IEA.
 DR GO; GO:0005198; F:Structural molecule activity; IEA.
 DR InterPro; IPR000328; Env_Gp41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR Pfam; PF00517; GP41; 1.
 KW AIDS; Coat protein; Envelope protein; Glycoprotein; Polypeptide;
 KW Transmembrane.
 SQ SEQUENCE 861 AA; 97670 MW; 8136732E44445B56 CRC64;

Query Match

Best Local Similarity 55.9%; Score 119; DB 2; Length 861;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 17 TRPNYKRRKRIHIGPGRAFYTTK 39
Db 302 TRPNYKRRKRIHIGPGRAFYTTK 324

RESULT 8

Q91191 PRELIMINARY; PRT; 162 AA.
AC 091191;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DE 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Subtype F;
RA MEDLINE=97225064; PubMed=9071437;
RA Apefret C., Louseert-Ajaka I., Collin G., Letourneur F., Duca M.,
RT "HIV-1 subtype F sequences cluster among Romanian children and
adults.";
RL AIDS Res. Hum. Retroviruses 13:363-365(1997).
DR HSPB; P05877; INO0.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0019028; C:Viral capsid; IEA.
DR GO; GO:0019031; C:Viral envelope; IEA.
DR InterPro; IPR000777; F:Structural molecule activity; IEA.
DR InterPro; IPR01056; Pept_S24_S26_C.
KW Pfam; PF00516; GP120; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 162
SQ SEQUENCE 162 AA; 18340 MW; 988PBC982FDFC6 CRC64;

Query Match

Best Local Similarity 53.1%; Score 113; DB 2; Length 162;
Matches 20; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 17 TRPNYKRRKRIHIGPGRAFYTTK 38
Db 13 TRPNYKRRKRIHIGPGRAFYTTK 34

RESULT 9

Q9YT94 PRELIMINARY; PRT; 108 AA.
AC 09YT94;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DE 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
GN Envelope glycoprotein (Fragment).
OS Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=9180162; PubMed=10082125; DOI=10.1089/08922299311385;
RA Roth W.W., Womack C., Newman C., Essex M., Bond V.C.;
RT "Phylogenetic examination of HIV type 1 glycoprotein 120-V3 sequences
in Patients from rural Georgia.";
RL AIDS Res. Hum. Retroviruses 15:399-403(1999).

DR EMBL; AF086997; AAC72226.1; -.
DR HSPB; P05877; INO0.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0019028; C:Viral capsid; IEA.
DR GO; GO:0019031; C:Viral envelope; IEA.
DR InterPro; IPR000777; F:Structural molecule activity; IEA.
DR Pfam; PF00516; GP120; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 12416 MW; A1E0413A5A97447A CRC64;

Query Match
Best Local Similarity 52.1%; Score 111; DB 2; Length 108;
Matches 20; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 17 TRPNYKRRKRIHIGPGRAFYTTK 39
Db 28 TRPNYKRRKRIHIGPGRAFYTTK 50

RESULT 10

Q85831 PRELIMINARY; PRT; 63 AA.
AC 085831;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DE 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
GN Envelope glycoprotein, v3 region (Fragment).
OS Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=95032920; PubMed=7946099;
RA Sabino F., Pan L.Z., Cheng-Mayer C., Mayer A.;
RT "Comparison of in vivo plasma and peripheral blood mononuclear cell
RT of tat and C2-V3 env regions.";
RL AIDS 8:901-909(1994).
DR EMBL; U00336; AAA57662.1; -.
DR HSPB; P20871; ICE4.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0019028; C:Viral capsid; IEA.
DR GO; GO:0019031; C:Viral envelope; IEA.
DR InterPro; IPR000777; F:Structural molecule activity; IEA.
DR InterPro; IPR007110; IG-1ike.
KW Pfam; PF00516; GP120; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 63
SQ SEQUENCE 63 AA; 6997 MW; 547895284E23E90C CRC64;

Query Match
Best Local Similarity 51.6%; Score 110; DB 2; Length 63;
Matches 20; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 14 MYATRPNNTRKSIHIGPGRAFYTTK 38
Db 27 IYCTRPNNTRKSIHIGPGRAFYTTK 51

RESULT 11

Q85837 PRELIMINARY; PRT; 63 AA.
AC 085837;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DE 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
GN Envelope glycoprotein, v3 region (Fragment).

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GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxId=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=95032920; PubMed=7946099;
RX Sabino E., Pan L.Z., Cheng-Mayer C., Mayer A.;
RT "Comparison of in vivo plasma and peripheral blood mononuclear cell
RT HIV-1 quasi-species to short-term tissue culture isolates: an analysis
RT of lat and C2-V3 env regions.";
RL AIDS 8:901-909(1994).
DR EMBL; U00342; AA57668.1; -.
DR HSSP; P20871; ICE4.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 1 1
FT NON_TER 63 63
SQ SEQUENCE 63 AA; 6997 MW; 547895284E23E90C CRC64;

Query Match 51.6%; Score 110; DB 2; Length 63;
Best Local Similarity 80.0%; Pred. No. 3.8e-08;
Matches 20; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 14 MYATRPVYNKRKHIGPGRAFYTT 38
Db 27 ICTRPVNNTRKSIHIGPGRAFYTT 51

RESULT 12
Q070454 PRELIMINARY; PRT; 70 AA.
AC Q070454;
DT 01-NOV-1996 (TEMBLrel. 01, Created)
DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein, v3 region (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxId=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=95127302; PubMed=7826703;
RX Futura Y., Bergstrom T., Norstrom G., Horal P.;
RT "HIV type 1 V3 sequence diversity in contact-traced Swedish couples at
RT the time of sexual transmission.";
RL AIDS Res. Hum. Retroviruses 10:1187-1189(1994).
RN [2]
RP SEQUENCE FROM N.A.
RA Mulder K.E.;
RL Submitted (JUN-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U10936; AAA66506.1; -.
DR HSSP; P20871; ICE4.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 1 1
FT NON_TER 70 70
SQ SEQUENCE 70 AA; 8016 MW; 0E34A35776A8E649 CRC64;

Query Match 51.6%; Score 110; DB 2; Length 63;
Best Local Similarity 80.0%; Pred. No. 3.8e-08;
Matches 20; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 14 MYATRPVYNKRKHIGPGRAFYTT 38
Db 27 ICTRPVNNTRKSIHIGPGRAFYTT 51

RESULT 13
Q070457 PRELIMINARY; PRT; 70 AA.
AC Q070457;
DT 01-NOV-1996 (TEMBLrel. 01, Created)
DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein, v3 region (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxId=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95127302; PubMed=7826703;
RA Futura Y., Bergstrom T., Norstrom G., Horal P.;
RT "HIV type 1 V3 sequence diversity in contact-traced Swedish couples at
RT the time of sexual transmission.";
RL AIDS Res. Hum. Retroviruses 10:1187-1189(1994).
RN [2]
RP SEQUENCE FROM N.A.
RA Mulder K.E.;
RL Submitted (JUN-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U10939; AAA66509.1; -.
DR HSSP; P20871; ICE4.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 1 1
FT NON_TER 70 70
SQ SEQUENCE 70 AA; 8016 MW; 0E34A35776A8E649 CRC64;

Query Match 51.6%; Score 110; DB 2; Length 70;
Best Local Similarity 80.0%; Pred. No. 4.3e-08;
Matches 20; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 14 MYATRPVYNKRKHIGPGRAFYTT 38
Db 4 ICTRPVNNTRKSIHIGPGRAFYTT 28

RESULT 14
Q093001 PRELIMINARY; PRT; 73 AA.
AC Q093001;
DT 01-NOV-1998 (TEMBLrel. 08, Created)
DT 01-NOV-1998 (TEMBLrel. 08, Last sequence update)
DT 01-JUN-2003 (TEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxId=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98334236; PubMed=9671221;
RA Bostable M.C., Merzouk A., Attalla M., Sadowski I.J.;
RT "Distinct clustering of HIV type 1 sequences derived from injection
RT versus noninjection drug users in Vancouver, Canada.";
RL AIDS Res. Hum. Retroviruses 14:917-919(1998).

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Best Local Similarity 80.0%; Pred. No. 4.3e-08;
Matches 20; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 14 MYATRPVYNKRKHIGPGRAFYTT 38
Db 4 ICTRPVNNTRKSIHIGPGRAFYTT 28

RESULT 13
Q070457 PRELIMINARY; PRT; 70 AA.
AC Q070457;
DT 01-NOV-1996 (TEMBLrel. 01, Created)
DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein, v3 region (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxId=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95127302; PubMed=7826703;
RA Futura Y., Bergstrom T., Norstrom G., Horal P.;
RT "HIV type 1 V3 sequence diversity in contact-traced Swedish couples at
RT the time of sexual transmission.";
RL AIDS Res. Hum. Retroviruses 10:1187-1189(1994).
RN [2]
RP SEQUENCE FROM N.A.
RA Mulder K.E.;
RL Submitted (JUN-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U10939; AAA66509.1; -.
DR HSSP; P20871; ICE4.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 1 1
FT NON_TER 70 70
SQ SEQUENCE 70 AA; 8016 MW; 0E34A35776A8E649 CRC64;

Query Match 51.6%; Score 110; DB 2; Length 70;
Best Local Similarity 80.0%; Pred. No. 4.3e-08;
Matches 20; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 14 MYATRPVYNKRKHIGPGRAFYTT 38
Db 4 ICTRPVNNTRKSIHIGPGRAFYTT 28

RESULT 14
Q093001 PRELIMINARY; PRT; 73 AA.
AC Q093001;
DT 01-NOV-1998 (TEMBLrel. 08, Created)
DT 01-NOV-1998 (TEMBLrel. 08, Last sequence update)
DT 01-JUN-2003 (TEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxId=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98334236; PubMed=9671221;
RA Bostable M.C., Merzouk A., Attalla M., Sadowski I.J.;
RT "Distinct clustering of HIV type 1 sequences derived from injection
RT versus noninjection drug users in Vancouver, Canada.";
RL AIDS Res. Hum. Retroviruses 14:917-919(1998).

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DR EMBL: AF058159; AAC15172.1; -.
 DR HSSP: P05877; INT0.
 DR GO: GO:0016021; C: integral to membrane; IEA.
 DR GO: GO:0019028; C: viral capsid; IEA.
 DR GO: GO:0019031; C: viral envelope; IEA.
 DR GO: GO:0005198; F: structural molecule activity; IEA.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 DR AIDS: Coat protein; Envelope protein; Glycoprotein; Transmembrane.
 FT NON_TER 1
 FT TER 1
 SQ SEQUENCE 73 AA; 8198 MW; 42E9F73F9FF355EB CRC64;

Query Match

Best Local Similarity 51.6%; Score 110; DB 2; Length 73;
 Matches 20; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 14 MYATRPVNNKRRKRIHIGPGRAPFTT 38
 DB 11 IYCTRPNNNTKRSIHIGPGRAPFTT 35

RESULT 15

O9WH03 PRELIMINARY; PRT; 136 AA.
 AC O9WH03;
 DT 01-NOV-1999 (T-EMBLrel. 12, Created)
 DT 01-NOV-1999 (T-EMBLrel. 12, Last sequence update)
 DE Envelope glycoprotein (Fragment).
 GN Name=env;
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN 11
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99252223; PubMed=10233993;
 RA Zhang P.F., Chen X., Fu D.W., Margolick J.B., Quinan G.V. Jr.;
 RT "Primary virus envelope cross-reactivity of the broadening
 RT neutralizing antibody response during early chronic human
 RT immunodeficiency virus type 1 infection.";
 RL J. Virol. 73:5225-5230 (1999).
 DR EMBL: AF130390; AAD3299.1; -.
 DR HSSP: P20871; ICE4.
 DR GO: GO:0016021; C: integral to membrane; IEA.
 DR GO: GO:0019028; C: viral capsid; IEA.
 DR GO: GO:0019031; C: viral envelope; IEA.
 DR GO: GO:0005198; F: structural molecule activity; IEA.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 DR AIDS: Coat protein; Envelope protein; Glycoprotein; Transmembrane.
 FT NON_TER 1
 FT TER 1
 SQ SEQUENCE 136 AA; 15370 MW; 3F47C47412B9C3A3 CRC64;

Query Match

Best Local Similarity 51.4%; Score 109.5; DB 2; Length 136;
 Matches 25; Conservative 2; Mismatches 10; Indels 1; Gaps 1;

OY 1 KQIINMVEYGVKMYATRPVNNKRRKRIHIGPGRAPFTT 38
 DB 5 KTIIVOLKEVVK-INCTRPNNNTKRSIHIGPGRAPFTT 41

Search completed: February 24, 2005, 07:31:04
 Job time: 179 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: February 24, 2005, 07:21:52 ; Search time 16 Seconds
(without alignments)
234.528 Million cell updates/sec

Title: US-10-009-473-2

Perfect score: 213

Sequence: 1 KQIIMMOEVGKAMYATRPNNYKRRKHIGRAFYTTK 39

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_79:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB ID	Description
1	128	60.1	859	1	VCLJMN
2	102	47.9	35	2	PC2295
3	102	47.9	110	2	A46410
4	102	47.9	847	2	T09448
5	102	47.9	847	2	S13289
6	101	47.4	77	2	S35848
7	101	47.4	77	2	S35815
8	101	47.4	77	2	S35816
9	99	46.5	35	2	PC2296
10	98	46.0	77	2	S35849
11	97	45.5	77	2	S35869
12	97	45.5	77	2	S35832
13	97	45.5	77	2	S35830
14	97	45.5	77	2	S35868
15	97	45.5	110	2	B46410
16	97	45.5	110	2	D46410
17	97	45.5	110	2	D46410
18	97	45.5	290	2	S25940
19	96	45.1	71	2	S42904
20	96	45.1	71	2	S42905
21	96	45.1	71	2	S42918
22	96	45.1	77	2	S35800
23	96	45.1	77	2	S35844
24	96	45.1	77	2	S35850
25	96	45.1	77	2	S35801
26	96	45.1	77	2	S35843
27	95.5	44.8	77	2	S35862
28	95	44.6	77	2	S35806
29	95	44.6	77	2	S35841

30	95	44.6	77	2	S35804	envelope protein -
31	94	44.1	77	2	S35808	envelope protein -
32	94	44.1	77	2	S35834	envelope protein -
33	94	44.1	77	2	S35831	envelope protein -
34	94	44.1	77	2	S35836	envelope protein -
35	94	44.1	77	2	S35835	envelope protein -
36	94	44.1	77	2	S35867	envelope protein -
37	94	44.1	77	2	S35809	envelope protein -
38	94	44.1	855	1	VCLJAZ	env polypeptide pr
39	93	43.7	71	2	S42915	env polypeptide -
40	93	43.7	71	2	S42899	env polypeptide -
41	93	43.7	71	2	S42913	env polypeptide -
42	93	43.7	71	2	S42914	env polypeptide -
43	93	43.7	74	2	S35814	envelope protein -
44	92	43.2	76	2	S35859	envelope protein -
45	92	43.2	77	2	S35820	envelope protein -

ALIGNMENTS

RESULT 1

VCLJMN env polypeptide precursor - human immunodeficiency virus type 1 (isolate MN)

N/Alternate names: coat polypeptide

C/Species: human immunodeficiency virus type 1, HIV-1

A/Note: host Homo sapiens (man)

C/Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #ext_change 16-Feb-1997

C/Accession: A28922

R/Guigo, C.; Guo, H.G.; Franchini, G.; Aldovini, A.; Collalti, E.; Farrell, K.; Wong-Scar

Virology 164, 531-536, 1988

A/Title: Envelope sequences of two new United States HIV-1 isolates.

A/Reference number: A28922; PMID:88219542; PMID:3369091

A/Accession: A28922

A/Molecule type: DNA

A/Residues: 1-859 <GUR>

C/Genetics:

A/Genes: env

C/Superfamily: type E retrovirus env polypeptide

C/Keywords: capsid protein; coat protein; glycoprotein; polypeptide; transmembrane protei

F/1-29/Domain: signal sequence #status predicted <Sig>

F/30-859/Product: env polypeptide #status predicted <Exp>

F/87,129,135,140,141,146,161,165,191,202,246,267,281,294,300,336,343,359,365,389,395,401,

Query Match 60.1%; Score 128; DB 1; Length 859;

Best Local Similarity 100.0%; Pred. No. 1.5e-09;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 TRPNYKRRKHIGRAFYTTK 39

DB 302 TRPNYKRRKHIGRAFYTTK 324

RESULT 2

PC2295 V3 domain peptide P4317 - human immunodeficiency virus type 1 (fragment)

C/Species: human immunodeficiency virus type 1, HIV-1

C/Date: 21-Feb-1995 #sequence_revision 05-Apr-1995 #ext_change 09-Jul-2004

C/Accession: PC2295

R/Shefer, K.; Soenherborg, A.; Steinberg, J.; Saelberg, M.

Biochem. Biophys. Res. Commun. 205, 1658-1664, 1994

A/Title: Rapid grouping of HIV-1 infection in subtypes A to E by V3 peptide serotyping ar

A/Reference number: PC2291; PMID:95110306; PMID:7811250

A/Accession: PC2295

A/Molecule type: protein

A/Residues: 1-35 <SHE>

C/Cross-references: UNIPROT:Q8JA61; UNIPROT:Q8JA72; UNIPROT:Q8JA67; UNIPROT:Q8JA75; UNIP

Query Match 47.9%; Score 102; DB 2; Length 35;

Best Local Similarity 86.4%; Pred. No. 2.2e-07;

Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 17 TRPNVNRKRRIHIGPGRAFYTT 38
 Db 2 TRPNNTTKSIHIGPGRAFYTT 23

RESULT 3

A46410
 envelope protein (V3 domain) - human immunodeficiency virus type 1 (fragment)
 C/Species: human immunodeficiency virus type 1, HIV-1
 C/Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
 R/McName: A46410
 Proc. Natl. Acad. Sci. U.S.A. 89, 10247-10251, 1992
 A/Title: Relationship of human immunodeficiency virus type 1 sequence heterogeneity to
 A/Reference number: A46410, MIDB:93066216, PMID:1438212
 A/Accession: A46410
 A/Status: preliminary; not compared with conceptual translation
 A/Molecule type: nucleic acid
 A/Residues: 1-110 <MCN>
 A/Cross-references: UNIPROT:Q9PY06
 A/Experimental source: subject S1
 A/Note: sequence extracted from NCBI backbone (NCBIP.117724)
 C/Superfamily: type E retrovirus env polypeptide

Query Match 47.9%; Score 102; DB 2; Length 110;
 Best Local Similarity 86.4%; Pred. No. 7.2e-07;
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 17 TRPNVNRKRRIHIGPGRAFYTT 38
 Db 38 TRPNNTTKSIHIGPGRAFYTT 59

RESULT 4

T09448
 envelope glycoprotein - human immunodeficiency virus type 1 (strain JREF)
 C/Species: human immunodeficiency virus type 1, HIV-1
 C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
 R/Pang, S.; Vinters, H.V.; Akashi, T.; O'Brien, W.A.; Chen, I.S.; Koyanagi, Y.; Namazie,
 A/Reference number: T09448
 A/Accession: T09448
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-847 <PAN>
 A/Cross-references: UNIPROT:Q75760; EMBL:U63632; NID:G1465777; PID:G1465781
 A/Genetic: env
 C/Superfamily: type E retrovirus env polypeptide

Query Match 47.9%; Score 102; DB 2; Length 847;
 Best Local Similarity 86.4%; Pred. No. 6e-06;
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 17 TRPNVNRKRRIHIGPGRAFYTT 38
 Db 294 TRPNNTTKSIHIGPGRAFYTT 315

RESULT 5

S13289
 env protein - human immunodeficiency virus type 1
 C/Species: human immunodeficiency virus type 1, HIV-1
 C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
 R/O'Brien, W.A.; Koyanagi, Y.; Namazie, A.; Zhao, J.O.; Diagne, A.; Idler, K.; Zack, J.A.
 A/Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp120
 A/Reference number: S13289, MUID:91043044, PMID:2172833
 A/Accession: S13289
 A/Status: preliminary
 A/Molecule type: DNA

A/Residues: 1-847 <OBR>
 A/Cross-references: UNIPROT:Q75760
 C/Superfamily: type E retrovirus env polypeptide

Query Match 47.9%; Score 102; DB 2; Length 847;
 Best Local Similarity 86.4%; Pred. No. 6e-06;
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 17 TRPNVNRKRRIHIGPGRAFYTT 38
 Db 294 TRPNNTTKSIHIGPGRAFYTT 315

RESULT 6

S35848
 envelope protein - human immunodeficiency virus type 1 (fragment)
 C/Species: human immunodeficiency virus type 1, HIV-1
 C/Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 09-Jul-2004
 R/Chiodi, F.
 A/Reference number: S35848
 A/Accession: S35848
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-77 <CHI>
 A/Cross-references: UNIPROT:Q7530; EMBL:Z23232; NID:G313607; PIDN:CAA80750.1; PID:G313
 C/Superfamily: type E retrovirus env polypeptide

Query Match 47.4%; Score 101; DB 2; Length 77;
 Best Local Similarity 86.4%; Pred. No. 6.8e-07;
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 17 TRPNVNRKRRIHIGPGRAFYTT 38
 Db 27 TRPNNTTKSIHIGPGRAFYTT 48

RESULT 7

S35815
 envelope protein - human immunodeficiency virus type 1 (fragment)
 C/Species: human immunodeficiency virus type 1, HIV-1
 C/Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 09-Jul-2004
 R/Chiodi, F.
 A/Reference number: S35815
 A/Accession: S35815
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-77 <CHI>
 A/Cross-references: UNIPROT:Q7494; EMBL:Z23193; NID:G313535; PIDN:CAA80714.1; PID:G31353
 C/Superfamily: type E retrovirus env polypeptide

Query Match 47.4%; Score 101; DB 2; Length 77;
 Best Local Similarity 86.4%; Pred. No. 6.8e-07;
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 17 TRPNVNRKRRIHIGPGRAFYTT 38
 Db 27 TRPNNTTKSIHIGPGRAFYTT 48

RESULT 8

S35816
 envelope protein - human immunodeficiency virus type 1 (fragment)
 C/Species: human immunodeficiency virus type 1, HIV-1
 C/Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 09-Jul-2004
 R/Chiodi, F.
 A/Reference number: S35816
 A/Accession: S35816
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-77 <CHI>
 A/Cross-references: UNIPROT:Q7494; EMBL:Z23193; NID:G313535; PIDN:CAA80714.1; PID:G31353
 C/Superfamily: type E retrovirus env polypeptide

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-77 <CHI>
A:Cross-references: UNIPROT:Q77495; EMBL:Z23194; NID:G31353; PIDN:CAA80715.1; PID:G3135
C:Superfamily: type E retrovirus env polypotein

Query Match 47.4%; Score 101; DB 2; Length 77;
Best Local Similarity 86.4%; Pred. No. 6.8e-07;

Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 17 TRPNYKRRKRIHIGPGRFYTT 38
Db 27 TRPNNTKRSIHIGPGRFYTT 48

RESULT 9

PC2296
V3 domain peptide P4346 - human immunodeficiency virus type 1 (fragment)

C:Species: human immunodeficiency virus type 1, HIV-1
C>Date: 21-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 09-Jul-2004

C:Accession: PC2296
R:Shereff, K.; Soenmerborg, A.; Steinberg, J.; Seelberg, M.

Biochem. Biophys. Res. Commun. 205, 1658-1664, 1994

A:Title: Rapid grouping of HIV-1 infection in subtypes A to E by V3 peptide serotyping

A:Reference number: PC2291; PMID:95110306; PMID:7811250

A:Accession: PC2296

A:Molecule type: protein

A:Residues: 1-35 <SHE>
A:Cross-references: UNIPROT:Q70826; UNIPROT:Q70831

C:Superfamily: type E retrovirus env polypotein

Query Match 46.5%; Score 99; DB 2; Length 35;
Best Local Similarity 81.8%; Pred. No. 5.7e-07;

Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 17 TRPNYKRRKRIHIGPGRFYTT 38
Db 2 TRPNNTKRSIHIGPGRFYTT 23

RESULT 10

S35849
envelope protein - human immunodeficiency virus type 1 (fragment)

C:Species: human immunodeficiency virus type 1, HIV-1
C>Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 09-Jul-2004

C:Accession: S35849
R:Chiodi, F.

submitted to the EMBL Data Library, June 1993

A:Reference number: S35800

A:Accession: S35849

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-77 <CHI>

A:Cross-references: UNIPROT:Q77531; EMBL:Z23233; NID:G313609; PIDN:CAA80751.1; PID:G3136
C:Superfamily: type E retrovirus env polypotein

Query Match 46.0%; Score 98; DB 2; Length 77;
Best Local Similarity 81.8%; Pred. No. 1.8e-06;

Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 17 TRPNYKRRKRIHIGPGRFYTT 38
Db 27 TRPNNTKRSIHIGPGRFYTT 48

RESULT 11

S35869
envelope protein - human immunodeficiency virus type 1 (fragment)

C:Species: human immunodeficiency virus type 1, HIV-1
C>Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 09-Jul-2004

C:Accession: S35869
R:Chiodi, F.

submitted to the EMBL Data Library, June 1993

A:Reference number: S35800

A:Accession: S35869

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-77 <CHI>

A:Cross-references: UNIPROT:Q77552; EMBL:Z23254; NID:G313650; PIDN:CAA80772.1; PID:G3136
C:Superfamily: type E retrovirus env polypotein

Query Match 45.5%; Score 97; DB 2; Length 77;
Best Local Similarity 81.8%; Pred. No. 2.4e-06;

Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 17 TRPNYKRRKRIHIGPGRFYTT 38
Db 27 TRPNNTKRSIHIGPGRFYAT 48

RESULT 12

S35832
envelope protein - human immunodeficiency virus type 1 (fragment)

C:Species: human immunodeficiency virus type 1, HIV-1
C>Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 09-Jul-2004

C:Accession: S35832; S35833
R:Chiodi, F.

submitted to the EMBL Data Library, June 1993

A:Reference number: S35800

A:Accession: S35832

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-77 <CHI>

A:Cross-references: UNIPROT:Q77514; UNIPROT:Q77514; EMBL:Z23214; NID:G313573; PIDN:CAA80
C:Superfamily: type E retrovirus env polypotein

Query Match 45.5%; Score 97; DB 2; Length 77;
Best Local Similarity 81.8%; Pred. No. 2.4e-06;

Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 17 TRPNYKRRKRIHIGPGRFYTT 38
Db 27 TRPNNTKRSIHIGPGRFYAT 48

RESULT 13

S35830
envelope protein - human immunodeficiency virus type 1 (fragment)

C:Species: human immunodeficiency virus type 1, HIV-1
C>Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 09-Jul-2004

C:Accession: S35830
R:Chiodi, F.

submitted to the EMBL Data Library, June 1993

A:Reference number: S35800

A:Accession: S35830

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-77 <CHI>

A:Cross-references: UNIPROT:Q77512; EMBL:Z23212; NID:G313569; PIDN:CAA80732.1; PID:G3135
C:Superfamily: type E retrovirus env polypotein

Query Match 45.5%; Score 97; DB 2; Length 77;
Best Local Similarity 81.8%; Pred. No. 2.4e-06;

Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 17 TRPNYKRRKRIHIGPGRFYTT 38
Db 27 TRPNNTKRSIHIGPGRFYAT 48

RESULT 14

S35868
envelope protein - human immunodeficiency virus type 1 (fragment)

C:Species: human immunodeficiency virus type 1, HIV-1
C>Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 09-Jul-2004

C:Accession: S35868; S35870

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 24, 2005, 07:27:03 ; Search time 131 Seconds
(without alignment)
97.423 Million cell updates/sec

Title: US-10-009-473-2

Perfect score: 213
Sequence: 1 KOIIMMOEVGKAMYATRPNNYKRRKHIGPRAFYTTK 39

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1380268 seqs, 327241040 residues

Total number of hits satisfying chosen parameters: 1380268

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	213	100.0	39	9	US-09-775-805-95
2	213	100.0	39	16	US-10-416-262B-2
3	213	100.0	39	16	US-10-753-339-91
4	202.5	95.1	40	9	US-09-989-284-1
5	202.5	95.1	40	16	US-09-956-940-17
6	202.5	95.1	40	16	US-10-416-262B-1
7	202.5	95.1	52	10	US-09-956-940-19
8	176	82.6	39	9	US-09-775-805-98
9	176	82.6	39	16	US-10-753-339-98
10	174.5	81.9	35	10	US-09-956-940-16
11	174.5	81.9	47	10	US-09-956-940-18
12	170	79.8	39	14	US-10-289-228-1
13	170	79.8	39	15	US-10-373-592-1

14	170	79.8	39	15	US-10-431-596-1	Sequence 1, Appl
15	169	79.3	39	14	US-10-289-228-3	Sequence 3, Appl
16	169	79.3	39	15	US-10-373-592-3	Sequence 3, Appl
17	169	79.3	39	15	US-10-431-596-3	Sequence 3, Appl
18	169	79.3	39	16	US-10-416-262B-4	Sequence 28, Appl
19	169	79.3	39	14	US-10-289-228-28	Sequence 28, Appl
20	165	77.5	39	15	US-10-373-592-28	Sequence 28, Appl
21	165	77.5	39	15	US-10-431-596-28	Sequence 51, Appl
22	164.5	77.2	38	14	US-10-289-228-51	Sequence 51, Appl
23	164.5	77.2	38	15	US-10-373-592-51	Sequence 51, Appl
24	164.5	77.2	38	15	US-10-373-592-70	Sequence 51, Appl
25	164.5	77.2	38	15	US-10-431-596-51	Sequence 51, Appl
26	164	77.0	39	14	US-10-289-228-25	Sequence 25, Appl
27	164	77.0	39	15	US-10-373-592-25	Sequence 25, Appl
28	164	77.0	39	15	US-10-431-596-25	Sequence 25, Appl
29	163	76.5	39	14	US-10-289-228-2	Sequence 2, Appl
30	163	76.5	39	14	US-10-289-228-24	Sequence 2, Appl
31	163	76.5	39	15	US-10-373-592-2	Sequence 2, Appl
32	163	76.5	39	15	US-10-373-592-24	Sequence 2, Appl
33	163	76.5	39	15	US-10-431-596-2	Sequence 2, Appl
34	163	76.5	39	15	US-10-431-596-24	Sequence 2, Appl
35	162	76.1	39	14	US-10-289-228-4	Sequence 4, Appl
36	162	76.1	39	15	US-10-373-592-4	Sequence 4, Appl
37	162	76.1	39	15	US-10-431-596-4	Sequence 4, Appl
38	162	76.1	39	16	US-10-416-262B-5	Sequence 5, Appl
39	160.5	75.4	38	14	US-10-289-228-53	Sequence 53, Appl
40	160.5	75.4	38	15	US-10-373-592-53	Sequence 53, Appl
41	160.5	75.4	38	15	US-10-373-592-80	Sequence 80, Appl
42	160.5	75.4	38	15	US-10-431-596-53	Sequence 53, Appl
43	160	75.1	39	14	US-10-289-228-13	Sequence 13, Appl
44	160	75.1	39	15	US-10-373-592-13	Sequence 13, Appl
45	160	75.1	39	15	US-10-431-596-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1
US-09-775-805-95
; Sequence 95, Application US/09775805
; Publication No. US20010036461A1
; GENERAL INFORMATION:
; APPLICANT: DUKE UNIVERSITY
; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS VACCINE
; FILE REFERENCE: 1579-548
; CURRENT APPLICATION NUMBER: US/09/775, 805
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 09/497,497
; PRIOR FILING DATE: 2000-09-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 95
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
; US-09-775-805-95

Query Match 100.0%; Score 213; DB 9; Length 39;
Best Local Similarity 100.0%; Pred. No. 4.7e-23;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KOIIMMOEVGKAMYATRPNNYKRRKHIGPRAFYTTK 39
DB 1 KOIIMMOEVGKAMYATRPNNYKRRKHIGPRAFYTTK 39

RESULT 2
US-10-416-262B-2
; Sequence 2, Application US/10416262B
; Publication No. US20040156620A1
; GENERAL INFORMATION:
; APPLICANT: American Cyanamid Company
; APPLICANT: Hagan, Michael

us-10-009-473-2.rapb

FILE OF INVENTION: Adjuvant Combination Formulations
 CURRENT APPLICATION NUMBER: US/10/416,262B
 PRIOR FILING DATE: 2003-05-08
 NUMBER OF SEQ ID NOS: 8
 SOFTWARE: PCT/US01/46943
 SEQ ID NO: 2 Patentln Version 3.2
 LENGTH: 39
 TYPE: PRT
 ORGANISM: Human immunodeficiency virus
 FEATURE: MISC FEATURE
 OTHER INFORMATION: Fragment of HIV
 US-10-416-262B-2

Query Match
 Best Local Similarity 100.0%; Score 213; DB 16; Length 39;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KOIIMMOEYKAMVATRPVYKRIHIGPRAFYTK 39
 DB 1 KOIIMMOEYKAMVATRPVYKRIHIGPRAFYTK 39

RESULT 3
 US-10-753-339-95
 Sequence 95, Application US/10753339
 Publication No. US20040197344A1
 GENERAL INFORMATION:
 APPLICANT: DUKE UNIVERSITY
 TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS VACCINE
 CURRENT REFERENCE: 1579-880
 PRIOR FILING DATE: 2004-01-09
 PRIOR APPLICATION NUMBER: US/10/753,339
 PRIOR FILING DATE: 2001-02-05
 PRIOR FILING DATE: 09/775,805
 NUMBER OF SEQ ID NOS: 09/497,497
 SOFTWARE: SEQ ID NOS: 107
 SEQ ID NO: 9 Patentln Ver. 2.1
 LENGTH: 39
 TYPE: PRT
 ORGANISM: Human immunodeficiency virus
 US-10-753-339-95

Query Match
 Best Local Similarity 100.0%; Score 213; DB 16; Length 39;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KOIIMMOEYKAMVATRPVYKRIHIGPRAFYTK 39
 DB 1 KOIIMMOEYKAMVATRPVYKRIHIGPRAFYTK 39

RESULT 4
 US-09-989-284-1
 Sequence 1, Application US/09989284
 Patent No. US20020127232A1
 GENERAL INFORMATION:
 APPLICANT: Salvatore V. Pizzo
 TITLE OF INVENTION: Immune Response Modulator
 FILE REFERENCE: Alpha-2-Macroglobulin Complex
 CURRENT APPLICATION NUMBER: US/09/989,284
 PRIOR FILING DATE: 2001-11-20
 NUMBER OF SEQ ID NOS: 1998-04-01
 SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO: 1
 LENGTH: 40
 TYPE: PRT
 ORGANISM: HIV
 US-09-989-284-1

Query Match
 Best Local Similarity 95.1%; Score 202.5; DB 9; Length 40;
 Matches 39; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
 QY 1 KOIIMMOEYKAMVATRPVYKRIHIGPRAFYTK 39
 DB 1 KOIIMMOEYKAMVATRPVYKRIHIGPRAFYTK 40

RESULT 5
 US-09-956-940-17
 Sequence 17, Application US/09956940
 Publication No. US20030022826A1
 GENERAL INFORMATION:
 APPLICANT: HAINES, BARTON F.
 TITLE OF INVENTION: USE OF SYNTHETIC PEPTIDES TO INDUCE TOLERANCE TO PATHOGENIC T AND B CELL EPITOPES OR CORRESPONDENCE ADDRESSES:
 ADDRESS: NIXON & VANDERHAYE P.C.
 STREET: 1100 NORTH GLEBE ROAD
 CITY: ARLINGTON
 STATE: VIRGINIA
 COUNTRY: U.S.A.
 ZIP: 22201-4714
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: Patentln Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/956,940
 FILING DATE: 12-Oct-2001
 CLASSIFICATION: <Unknown>
 APPLICATION DATA:
 FILING DATE: US/08/460,673
 FILING DATE: <Unknown>
 APPLICATION NUMBER: US 08/015,987
 FILING DATE: 10-FEB-1993
 APPLICATION NUMBER: US 07/833,429
 FILING DATE: 10-FEB-1992
 APPLICATION NUMBER: US 07/591,109
 FILING DATE: 01-OCT-1990
 APPLICATION NUMBER: US 07/093,854
 ATTORNEY/AGENT INFORMATION:
 NAME: WILSON, MARY J.
 REGISTRATION NUMBER: 32,955
 TELECOMMUNICATIONS INFORMATION:
 TELEPHONE: (703) 816-4100
 TELEFAX: (703) 816-4100
 INFORMATION FOR SEQ ID NO: 17:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 40 amino acids
 STRANDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 17:

Query Match
 Best Local Similarity 95.1%; Score 202.5; DB 10; Length 40;
 Matches 39; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

US-09-956-940-17

Qy 1 KOIINMOEVGKAMYA-TRPNYKRRRIHIGGRAFYTTK 39
Db 1 KOIINMOEVGKAMYACTRPNYKRRRIHIGGRAFYTTK 40

RESULT 6
US-10-416-262B-1
; Sequence 1, Application US/10416262B
; Publication No. US20040156620A1
; GENERAL INFORMATION:
; APPLICANT: American Cyanamid Company
; APPLICANT: Hagan, Michael
; TITLE OF INVENTION: Adjutant Combination Formulations
; FILE REFERENCE: AM100449
; CURRENT APPLICATION NUMBER: US/10/416,262B
; PRIOR APPLICATION NUMBER: PCT/US01/46943
; PRIOR FILING DATE: 2001-10-08
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 1
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
; FEATURE:
; NAME/KEY: MISC FEATURE
; OTHER INFORMATION: Fragment of HIV
US-10-416-262B-1

Query Match 95.1%; Score 202.5; DB 16; Length 40;
Best Local Similarity 97.5%; Pred. No. 1,6e-21;
Matches 39; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 KOIINMOEVGKAMYA-TRPNYKRRRIHIGGRAFYTTK 39
Db 1 KOIINMOEVGKAMYACTRPNYKRRRIHIGGRAFYTTK 40

RESULT 7
US-09-956-940-19
; Sequence 19, Application US/09956940
; Publication No. US20030022826A1
; GENERAL INFORMATION:
; APPLICANT: HAYNES, BARTON F.
; TITLE OF INVENTION: USE OF SYNTHETIC PEPTIDES TO INDUCE
; TOLERANCE TO PATHOGENIC T AND B CELL EPITOPES OF
; AUTOANTIGENS OR INFECTIOUS AGENTS
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/956,940
; FILING DATE: 12-Oct-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,673
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/015,987
; FILING DATE: 10-FEB-1993
; APPLICATION NUMBER: US 07/833,429
; FILING DATE: 10-FEB-1992
; APPLICATION NUMBER: US 07/591,109

; FILING DATE: 01-OCT-1990
; APPLICATION NUMBER: US 07/093,854
; FILING DATE: 08-SEP-1987
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 1579-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; TELEX: 200797 NIXN UR
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-956-940-19

Query Match 95.1%; Score 202.5; DB 10; Length 52;
Best Local Similarity 97.5%; Pred. No. 2,1e-21;
Matches 39; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 KOIINMOEVGKAMYA-TRPNYKRRRIHIGGRAFYTTK 39
Db 13 KOIINMOEVGKAMYACTRPNYKRRRIHIGGRAFYTTK 52

RESULT 8
US-09-775-805-98
; Sequence 98, Application US/09775805
; Publication No. US20010036461A1
; GENERAL INFORMATION:
; APPLICANT: DUKE UNIVERSITY
; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS VACCINE
; FILE REFERENCE: 1579-548
; CURRENT APPLICATION NUMBER: US/09/775,805
; PRIOR APPLICATION NUMBER: 2001-02-05
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 98
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-09-775-805-98

Query Match 82.6%; Score 176; DB 9; Length 39;
Best Local Similarity 84.2%; Pred. No. 9,5e-18;
Matches 32; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KOIINMOEVGKAMYATRPNNYKRRRIHIGGRAFYTT 38
Db 1 KOIINMOEVGKAMYATRPNNYKRRRIHIGGRAFYTT 38

RESULT 9
US-10-753-339-98
; Sequence 98, Application US/10753339
; Publication No. US20040197344A1
; GENERAL INFORMATION:
; APPLICANT: DUKE UNIVERSITY
; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS VACCINE
; FILE REFERENCE: 1579-880
; CURRENT APPLICATION NUMBER: US/10/753,339
; PRIOR APPLICATION NUMBER: 2004-01-09
; PRIOR FILING DATE: 09/775,805
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 09/497,497
; PRIOR FILING DATE: 2000-02-04

NUMBER OF SEQ ID NOS: 107
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 98
LENGTH: 39
TYPE: PRT
ORGANISM: Human immunodeficiency virus
US-10-753-339-98

Query Match
Best Local Similarity 82.6%; Score 176; DB 16; Length 39;
Matches 32; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 KOIIMMOEYVGKAMVATRPYNNKRRKRIHIGPRAFYTT 38
Db 1 KOIIMMOEYVGKAMVATRPYNNKRRKRIHIGPRAFYTT 38

RESULT 10

US-09-956-940-16
Sequence 16, Application US/09956940
Publication No. US20030022826A1
GENERAL INFORMATION:

APPLICANT: HAYNES, BARTON F.
TITLE OF INVENTION: USE OF SYNTHETIC PEPTIDES TO INDUCE

TOLERANCE TO PATHOGENIC T AND B CELL EPITOPES OF
AUTOANTIGENS OR INFECTIOUS AGENTS

NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESSES:

ADDRESSEE: NIXON & VANDERHAYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON

STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/956,940
FILING DATE: 12-Oct-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/460,673
FILING DATE: <Unknown>

APPLICATION NUMBER: US 08/015,987
FILING DATE: 10-FEB-1993
APPLICATION NUMBER: US 07/833,429

FILING DATE: 10-FEB-1992
APPLICATION NUMBER: US 07/591,109
FILING DATE: 01-OCT-1990

APPLICATION NUMBER: US 07/093,854
FILING DATE: 08-SEP-1987
ATTORNEY/AGENT INFORMATION:

NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 1579-5

TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100

TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 16:

US-09-956-940-16

Query Match 81.9%; Score 174.5; DB 10; Length 35;

Best Local Similarity 97.1%; Pred. No. 1.4e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 KOIIMMOEYVGKAMVATRPYNNKRRKRIHIGPRA 34
Db 1 KOIIMMOEYVGKAMVATRPYNNKRRKRIHIGPRA 35

RESULT 11

US-09-956-940-18
Sequence 18, Application US/09956940
Publication No. US20030022826A1
GENERAL INFORMATION:

APPLICANT: HAYNES, BARTON F.
TITLE OF INVENTION: USE OF SYNTHETIC PEPTIDES TO INDUCE

TOLERANCE TO PATHOGENIC T AND B CELL EPITOPES OF
AUTOANTIGENS OR INFECTIOUS AGENTS

NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESSES:

ADDRESSEE: NIXON & VANDERHAYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON

STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/956,940
FILING DATE: 12-Oct-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/460,673
FILING DATE: <Unknown>

APPLICATION NUMBER: US 08/015,987
FILING DATE: 10-FEB-1993
APPLICATION NUMBER: US 07/833,429

FILING DATE: 10-FEB-1992
APPLICATION NUMBER: US 07/591,109
FILING DATE: 01-OCT-1990

APPLICATION NUMBER: US 07/093,854
FILING DATE: 08-SEP-1987
ATTORNEY/AGENT INFORMATION:

NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 1579-5

TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100

TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 18:

SEQUENCE CHARACTERISTICS:
LENGTH: 47 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 18:

US-09-956-940-18

Query Match 81.9%; Score 174.5; DB 10; Length 47;

Best Local Similarity 97.1%; Pred. No. 1.9e-17;
Matches 34; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 KOIIMMOEYVGKAMVATRPYNNKRRKRIHIGPRA 34
Db 13 KOIIMMOEYVGKAMVATRPYNNKRRKRIHIGPRA 47

RESULT 12

```
US-10-289-228-1
; Sequence 1, Application US/10289228
; Publication No. US20030147888A1
; GENERAL INFORMATION:
; APPLICANT: HAYNES, BARTON F.
; APPLICANT: KORBER, BETTE T.
; APPLICANT: DE LORIMIER, ROBERT M.
; TITLE OF INVENTION: POLYVALENT IMMUNOGEN
; FILE REFERENCE: 1579-759
; CURRENT APPLICATION NUMBER: US/10/289,228
; CURRENT FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: 60/331,036
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Human Immunodeficiency Virus
US-10-289-228-1

Query Match      79.8%; Score 170; DB 14; Length 39;
Best Local Similarity 79.5%; Pred. No. 6.9e-17;
Matches 31; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy      1 KOIINMOEVGKAMYATRPNNYKRIHIGPGRAFYTTK 39
Db      1 KOIINMOEVGKAMYATRPNNYKRIHIGPGRAFYTTK 39

RESULT 13
US-10-373-592-1
; Sequence 1, Application US/10373592
; Publication No. US20040001851A1
; GENERAL INFORMATION:
; APPLICANT: HAYNES, BARTON F.
; APPLICANT: KORBER, BETTE T.
; APPLICANT: DE LORIMIER, ROBERT M.
; TITLE OF INVENTION: POLYVALENT IMMUNOGEN
; FILE REFERENCE: 1579-785
; CURRENT APPLICATION NUMBER: US/10/373,592
; CURRENT FILING DATE: 2003-02-26
; PRIOR APPLICATION NUMBER: 10/289,228
; PRIOR FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: 60/331,036
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-373-592-1

Query Match      79.8%; Score 170; DB 15; Length 39;
Best Local Similarity 79.5%; Pred. No. 6.9e-17;
Matches 31; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy      1 KOIINMOEVGKAMYATRPNNYKRIHIGPGRAFYTTK 39
Db      1 KOIINMOEVGKAMYATRPNNYKRIHIGPGRAFYTTK 39

RESULT 14
US-10-431-596-1
; Sequence 1, Application US/10431596
; Publication No. US20040086506A1
; GENERAL INFORMATION:
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; APPLICANT: HAYNES, BARTON F.
; APPLICANT: KORBER, BETTE T.
; APPLICANT: DE LORIMIER, ROBERT M.
; APPLICANT: LIAO, HUA-XIN
; TITLE OF INVENTION: POLYVALENT IMMUNOGEN
; FILE REFERENCE: 1579-813
; CURRENT APPLICATION NUMBER: US/10/431,596
; CURRENT FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: 10/373,592
; PRIOR FILING DATE: 2003-02-26
; PRIOR APPLICATION NUMBER: 10/289,228
; PRIOR FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: 60/331,036
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Human Immunodeficiency Virus
US-10-431-596-1

Query Match      79.8%; Score 170; DB 15; Length 39;
Best Local Similarity 79.5%; Pred. No. 6.9e-17;
Matches 31; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy      1 KOIINMOEVGKAMYATRPNNYKRIHIGPGRAFYTTK 39
Db      1 KOIINMOEVGKAMYATRPNNYKRIHIGPGRAFYTTK 39
```

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RESULT 15
US-10-289-228-3
; Sequence 3, Application US/10289228
; Publication No. US20030147888A1
; GENERAL INFORMATION:
; APPLICANT: HAYNES, BARTON F.
; APPLICANT: KORBER, BETTE T.
; APPLICANT: DE LORIMIER, ROBERT M.
; TITLE OF INVENTION: POLYVALENT IMMUNOGEN
; FILE REFERENCE: 1579-759
; CURRENT APPLICATION NUMBER: US/10/289,228
; CURRENT FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: 60/331,036
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Human Immunodeficiency Virus
US-10-289-228-3

Query Match      79.3%; Score 169; DB 14; Length 39;
Best Local Similarity 79.5%; Pred. No. 9.5e-17;
Matches 31; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy      1 KOIINMOEVGKAMYATRPNNYKRIHIGPGRAFYTTK 39
Db      1 KOIINMOEVGKAMYATRPNNYKRIHIGPGRAFYTTK 39

Search completed: February 24, 2005, 07:34:09
Job time : 132 secs
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